

SEQUENCE LISTING



<110> Smith, Leonard A.
Byrne, Michael P.
Middlebrook, John L.
Lapenotiere, Hugh
Clayton, Michael A.
Brown, Douglas R.

<120> RECOMBINANT VACCINE AGAINST BOTULINUM
NEUROTOXIN

<130> A33626-A 067252.0107

<140> 09/910,186

<141> 2001-07-20

<150> 09/611,419

<151> 2000-07-06

<150> PCT/US00/12890

<151> 2000-05-12

<150> 60/133,865

<151> 1999-05-12

<150> 60/133,866

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<150> 60/133,869

<151> 1999-05-12

<150> 60/146,192

<151> 1999-07-29

<150> 08/123,975

<151> 1993-09-21

<160> 44

<170> FastSEQ for Windows Version 4.0

<210> 1

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTA Hc

<400> 1

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cgtggtacca aattcatcat caagaaatac gcgtctggtg acaaggacaa tatcgttcgc 960
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aacaatatcg ctaaactggt tgcttccaac tgggtacaatc gtcagatcga acgttctct 1260
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ctgtaagaat tc                                     1332

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<210> 2

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 2

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Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
 20           25           30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
 35           40           45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
 50           55           60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
 65           70           75           80
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
 85           90           95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
 100          105          110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
 115          120          125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
 130          135          140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
 145          150          155          160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
 165          170          175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn

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ccgaacaaat acgttgacgt caacaatgta ggtatccgcg gttacatgta cctgaaaggt 840
ccgcgtgggt ctgttatgac taccaacatc tacctgaact ctccctgta ccgtgggtacc 900
aaattcatca tcaagaaata cgcgtctggt aacaaggaca atatcggtcg caacaatgat 960
cgtgtatata tcaatgttgt agttaagaac aaagaatacc gtctggctac caatgcttct 1020
caggctgggt tagaaaagat cttgtctgct ctggaaatcc cggacgttgg taatctgtct 1080
caggtagttg taatgaaatc caagaacgac cagggtatca ctaacaaatg caaaatgaat 1140
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gctaaactgg ttgcttccaa ctggtacaat cgtcagatcg aacgttcctc tcgcactctg 1260
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<210> 4

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

<400> 4

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Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
 20          25          30
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
 35          40          45
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
 50          55          60
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
 65          70          75          80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
 85          90          95
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
100          105          110
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
115          120          125
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
130          135          140
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
145          150          155          160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
165          170          175
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
180          185          190
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
195          200          205
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
210          215          220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
225          230          235          240
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
245          250          255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
260          265          270
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
275          280          285

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Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala
290						295					300				
Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile
305					310					315					320
Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser
				325					330					335	
Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val
			340					345					350		
Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly
	355						360					365			
Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp
370						375					380				
Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val
385					390					395					400
Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu
				405					410					415	
Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu	Arg
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<210> 5
 <211> 1326
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

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 atcaacatcg gttctaaagt taacttcgat ccgatcgaca agaatcagat ccagctgttc 180
 aatctggaat cttccaaaat cgaagttatc ctgaagaatg ctatcgtata caactctatg 240
 tacgaaaact tctccacctc cttctggatc cgtatcccga aatacttcaa ctccatctct 300
 ctgaacaatg aatacaccat catcaactgc atggaaaaca attctgggtg gaaagtatct 360
 ctgaactacg gtgaaatcat ctggactctg caggacactc aggaaatcaa acagcgtgtt 420
 gtattcaaat actctcagat gatcaacatc tctgactaca tcaatcgctg gatcttcgtt 480
 accatcacca acaatcgtct gaataactcc aaaatctaca tcaacggccg tctgatcgac 540
 cagaaaccga tctccaatct gggtaacatc cacgcttcta ataacatcat gttcaaactg 600
 gacggttgtc gtgacactca ccgctacatc tggatcaaat acttcaatct gttcgacaaa 660
 gaactgaacg aaaaagaaat caaagacctg tacgacaacc agtccaattc tggatatctg 720
 aaagacttct ggggtgacta cctgcagtac gacaaaccgt actacatgct gaatctgtac 780
 gatccgaaca aatacgttga cgtcaacaat gtaggtatcc gcggttacat gtacctgaaa 840
 ggtccgcgtg gttctgttat gactaccaac atctacctga actcttcctt gtaccgtggt 900
 accaaattca tcatcaagaa atacgcgtct ggtacaagg acaatatcgt tcgcaacaat 960
 gatcgtgtat acatcaatgt tgtagttaag aacaaagaat accgtctggc taccaatgct 1020
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 aatctgcagg acaacaatgg taacgatatc ggtttcatcg gtttccacca gttcaacaat 1200
 atcgctaaac tgggtgcttc caactggtac aatcgtcaga tcgaacgttc ctctcgact 1260
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<210> 6
 <211> 435

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hc

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			20					25					30		
Tyr	Ala	Ser	Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile
		35					40					45			
Asp	Lys	Asn	Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu
	50					55					60				
Val	Ile	Leu	Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe
65					70					75					80
Ser	Thr	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser
			85						90					95	
Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly
			100					105					110		
Trp	Lys	Val	Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp
	115						120					125			
Thr	Gln	Glu	Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile
	130					135					140				
Asn	Ile	Ser	Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn
145					150					155					160
Asn	Arg	Leu	Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp
			165						170					175	
Gln	Lys	Pro	Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile
			180					185					190		
Met	Phe	Lys	Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile
	195						200					205			
Lys	Tyr	Phe	Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys
	210					215					220				
Asp	Leu	Tyr	Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp
225					230					235					240
Gly	Asp	Tyr	Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr
			245						250				255		
Asp	Pro	Asn	Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr
		260						265					270		
Met	Tyr	Leu	Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr
	275						280					285			
Leu	Asn	Ser	Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr
	290					295					300				
Ala	Ser	Gly	Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr
305					310					315					320
Ile	Asn	Val	Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala
			325						330					335	
Ser	Gln	Ala	Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp
		340						345					350		
Val	Gly	Asn	Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln
	355					360						365			
Gly	Ile	Thr	Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn
	370					375					380				
Asp	Ile	Gly	Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu

385		390		395		400									
Val	Ala	Ser	Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr
			405						410					415	
Leu	Gly	Cys	Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu
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Arg	Pro	Leu													
		435													

<210> 7
 <211> 1341
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hc

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 tacaacatcc gtgaagacat ctctgaatac atcaatcgct gggtcttcgt taccatcacc 480
 aataacctga acaatgctaa aatctacatc aacggtaaac tggaatctaa taccgacatc 540
 aaagacatcc gtgaagttat cgctaacggt gaaatcatct tcaaactgga cgggtgacatc 600
 gatcgtaccc agttcatctg gatgaaatac ttctccatct tcaacaccga actgtctcag 660
 tccaatatcg aagaacggta caagatccag tcttactccg aataacctgaa agactttctgg 720
 ggtaatccgc tgatgtacaa caaagaatac tatatgttca atgctggtaa caagaactct 780
 tacatcaaac tgaagaaga ctctccgggt ggtgaaatcc tgactcgttc caaatacaac 840
 cagaactcta aatacatcaa ctaccgcgac ctgtacatcg gtgaaaagtt catcatccgt 900
 cgcaaactta actctcagtc catcaatgat gacatcgtac gtaaagaaga ctacatctac 960
 ctggactttc tcaacctgaa tcaggaatgg cgtgtataca cctacaagta cttcaagaaa 1020
 gaagaagaaa agcttttctc ggctccgac tctgattccg acgaactcta caacaccatc 1080
 cagatcaaag aatacgacga acagccgacc tactcttgcc agctgctggt caagaaagat 1140
 gaagaatcta ctgacgaaat cgggtctgatc ggtatccacc gtttctacga atctggtatc 1200
 gtattcgaag aatacaaaga ctacttctgc atctccaaat ggtacctgaa ggaagttaaa 1260
 cgcaaaccgt acaacctgaa actggggtgc aattggcagt tcatcccgaag agacgaaggt 1320
 tggaccgaat agtaagaatt c 1341

<210> 8
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTB Hc

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 20 25 30
 Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe

	35					40				45					
Lys	Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln
	50					55					60				
Asn	Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp
65					70					75				80	
Ile	Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His
				85					90					95	
Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys
		100						105					110		
Ile	Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn
		115					120					125			
Gly	Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile
	130					135					140				
Ser	Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu
145				150						155					160
Asn	Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp
			165					170					175		
Ile	Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	Gly	Glu	Ile	Ile	Phe	Lys
		180					185						190		
Leu	Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe
	195					200						205			
Ser	Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr
	210					215					220				
Lys	Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro
225					230					235					240
Leu	Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn
			245						250					255	
Ser	Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr
		260					265						270		
Arg	Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu
		275				280						285			
Tyr	Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser
	290					295					300				
Ile	Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	Tyr	Ile	Tyr	Leu	Asp	Phe
305				310						315					320
Phe	Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	Thr	Tyr	Lys	Tyr	Phe	Lys
			325						330					335	
Lys	Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile	Ser	Asp	Ser	Asp	Glu
		340					345					350			
Leu	Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr
		355				360						365			
Ser	Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile
	370					375					380				
Gly	Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu
385					390					395					400
Glu	Tyr	Lys	Asp	Tyr	Phe	Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val
			405						410					415	
Lys	Arg	Lys	Pro	Tyr	Asn	Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile
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Pro	Lys	Asp	Glu	Gly	Trp	Thr	Glu								
	435					440									

<210> 9

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTC1 Hc

<400> 9

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cgtaagaaca ccttggtcga cacctccggt tacaacgccg aggtctccga ggaggggtgac 180
gtccagctga acccaatctt cccattcgac ttcaagctgg gttcctccgg tgaggacaga 240
ggtaagggtca tcgtcaccca gaacgagaac atcgtctaca actccatgta cgagtccttc 300
tccatctcct tctggatcag aatcaacaag tgggtctcca acttgccagg ttacaccatc 360
atcgactccg tcaagaacaa ctccgggttg tccatcggta tcactctcaa cttcctgggtc 420
ttcaccctga agcagaacga ggactccgag cagtccatca acttctccta cgacatctcc 480
aacaacgctc ctgggttaca caagtgggtt ttcgtcaccc tcaccaacaa catgatgggt 540
aacatgaaga tctacatcaa cggtaagctg atcgacacca tcaagggtcaa ggagttgacc 600
ggtatcaact tctccaagac catcaccttc gagatcaaca agatcccaga caccgggtctg 660
atcacctccg actccgacaa catcaacatg tggatccgtg acttctacat cttcgccaag 720
gagttggacg gtaaggacat caacatcctg ttcaactcct tgcagtacac caacgtcgtc 780
aaggactact ggggtaacga cctgagatac aacaaggagt actacatggt caacatcgac 840
tacttgaaca gatacatgta cgccaactcc agacagatcg tcttcaacac cagacgtaac 900
aacaacgact tcaacgaggg ttacaagatc atcatcaagc gtatcagagg taacaccaac 960
gacaccagag tcagaggtgg tgacatcctg tacttcgaca tgactatcaa caacaaggcc 1020
tacaacctgt tcatgaagaa cgagaccatg tacgccgaca accactccac cgaggacatc 1080
tacgccatcg gtctgctgta gcagaccaag gacatcaacg acaacatcat cttccagatc 1140
cagccaatga acaacactta ctactacgtt tcccagatct tcaagtccaa cttcaacgggt 1200
gagaacatct ccggtatctg ttccatcgggt acctacagat tccgtctggg tgggtgactgg 1260
tacagacaca actacttgggt tccaactgtc aagcagggta actacgctc cttgctggag 1320
tccacttcca cccactgggg attcgtccca gtctccgagt aataggaatt c 1371
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<210> 10

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTC1 Hc

<400> 10

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Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu
 1           5           10           15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
      20           25           30
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
      35           40           45
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
      50           55           60
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
      65           70           75           80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
      85           90           95
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
      100          105          110
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
      115          120          125
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
      130          135          140
```

Asp	Ser	Glu	Gln	Ser	Ile	Asn	Phe	Ser	Tyr	Asp	Ile	Ser	Asn	Asn	Ala
145					150					155					160
Pro	Gly	Tyr	Asn	Lys	Trp	Phe	Phe	Val	Thr	Val	Thr	Asn	Asn	Met	Met
				165						170					175
Gly	Asn	Met	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Ile	Asp	Thr	Ile	Lys
			180					185					190		
Val	Lys	Glu	Leu	Thr	Gly	Ile	Asn	Phe	Ser	Lys	Thr	Ile	Thr	Phe	Glu
		195					200					205			
Ile	Asn	Lys	Ile	Pro	Asp	Thr	Gly	Leu	Ile	Thr	Ser	Asp	Ser	Asp	Asn
	210					215					220				
Ile	Asn	Met	Trp	Ile	Arg	Asp	Phe	Tyr	Ile	Phe	Ala	Lys	Glu	Leu	Asp
	225				230					235					240
Gly	Lys	Asp	Ile	Asn	Ile	Leu	Phe	Asn	Ser	Leu	Gln	Tyr	Thr	Asn	Val
				245					250					255	
Val	Lys	Asp	Tyr	Trp	Gly	Asn	Asp	Leu	Arg	Tyr	Asn	Lys	Glu	Tyr	Tyr
			260					265					270		
Met	Val	Asn	Ile	Asp	Tyr	Leu	Asn	Arg	Tyr	Met	Tyr	Ala	Asn	Ser	Arg
		275					280					285			
Gln	Ile	Val	Phe	Asn	Thr	Arg	Arg	Asn	Asn	Asn	Asp	Phe	Asn	Glu	Gly
	290					295					300				
Tyr	Lys	Ile	Ile	Ile	Lys	Arg	Ile	Arg	Gly	Asn	Thr	Asn	Asp	Thr	Arg
	305				310					315					320
Val	Arg	Gly	Gly	Asp	Ile	Leu	Tyr	Phe	Asp	Met	Thr	Ile	Asn	Asn	Lys
				325					330					335	
Ala	Tyr	Asn	Leu	Phe	Met	Lys	Asn	Glu	Thr	Met	Tyr	Ala	Asp	Asn	His
			340					345					350		
Ser	Thr	Glu	Asp	Ile	Tyr	Ala	Ile	Gly	Leu	Arg	Glu	Gln	Thr	Lys	Asp
		355					360					365			
Ile	Asn	Asp	Asn	Ile	Ile	Phe	Gln	Ile	Gln	Pro	Met	Asn	Asn	Thr	Tyr
	370					375					380				
Tyr	Tyr	Ala	Ser	Gln	Ile	Phe	Lys	Ser	Asn	Phe	Asn	Gly	Glu	Asn	Ile
	385			390						395					400
Ser	Gly	Ile	Cys	Ser	Ile	Gly	Thr	Tyr	Arg	Phe	Arg	Leu	Gly	Gly	Asp
				405					410					415	
Trp	Tyr	Arg	His	Asn	Tyr	Leu	Val	Pro	Thr	Val	Lys	Gln	Gly	Asn	Tyr
			420					425					430		
Ala	Ser	Leu	Leu	Glu	Ser	Thr	Ser	Thr	His	Trp	Gly	Phe	Val	Pro	Val
		435					440					445			
Ser	Glu														
	450														

<210> 11

<211> 1374

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTD Hc

<400> 11

gaattcacga	tgcgtttgaa	ggctaaggctc	aacgagtcct	tcgagaacac	catgccattc	60
aacatcttct	cctacaccaa	caactccttg	ttgaaggaca	tcatacaacga	gtacttcaac	120
tccatcaacg	actccaagat	cttgctcctg	cagaacaaga	agaacgcctt	ggctcgacacc	180
tccggttaca	acgccgaggt	cagagtcggt	gacaacgtcc	agttgaacac	catctacacc	240
aacgacttca	agttgtcctc	ttccggtgac	aagatcatcg	tcaacttgaa	caacaacatc	300
ttgtactccg	ccatctacga	gaactcctct	gtctccttct	ggatcaagat	ctccaaggac	360

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ttgaccaact cccacaacga gtacaccatc atcaactcca tcgagcagaa ctccggttgg 420
aagttgtgta tccgtaacgg taacatcgag tggatcttgc aggacgtcaa ccgtaagtac 480
aagtccttga tcttcgacta ctccgagtc ttgtcccaca ccggttacac caacaagtgg 540
ttcttcgtca ccatcaccaa caacatcatg gggttacatga agttgtacat caacggtgag 600
ttgaagcagt cccagaagat cgaggacctg gacgaggtca agctggacaa gaccatcgtc 660
ttcgggtatcg acgagaacat cgacgagAAC cagatgttgt ggatccgtga cttcaacatc 720
ttctccaagg agctgtccaa cgaggacatc aacatcgtct acgaggggtca gatcctgagg 780
aacgtcatca aggactactg gggtaaccca ctgaagttcg acaccgagta ctacatcatc 840
aacgacaact acatcgaccg ttacatcgcc ccagagtcca acgtcctggc cctgggtccag 900
taccctgacc gttccaagct gtacaccggt aaccctatca ccatcaagtc cgtctccgac 960
aagaaccctt actcccgtat cctgaacggt gacaacatca tctgcacat gctgtacaac 1020
tcccgtaaagt acatgatcat ccgtgacacc gacaccatct acgccacca ggggtggtgac 1080
tggtcccaga actgtgtcta cgccctgaag ctgcagtcca acctgggtaa ctacggtatc 1140
ggatcttctt ccatcaagaa catcgtctcc aagaacaagt actgctcca gatcttctcc 1200
tccttccgtg agaacacat gctgctggcc gacatctaca agccttggcg tttctccttc 1260
aagaacgctt acactcctgt cgccgtcacc aactacgaga ccaagctgct gtccacctcc 1320
tccttctgga agttcatctc ccgtgaccca gggtgggtcg agtaatagga attc 1374

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<210> 12

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hc

<400> 12

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Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
1          5          10          15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
20          25          30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
35          40          45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
50          55          60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65          70          75          80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
85          90          95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
100         105         110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
115         120         125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
130         135         140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145         150         155         160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
165         170         175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
180         185         190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
195         200         205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
210         215         220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys

```

225		230		235		240									
Glu	Leu	Ser	Asn	Glu	Asp	Ile	Asn	Ile	Val	Tyr	Glu	Gly	Gln	Ile	Leu
			245						250					255	
Arg	Asn	Val	Ile	Lys	Asp	Tyr	Trp	Gly	Asn	Pro	Leu	Lys	Phe	Asp	Thr
		260						265					270		
Glu	Tyr	Tyr	Ile	Ile	Asn	Asp	Asn	Tyr	Ile	Asp	Arg	Tyr	Ile	Ala	Pro
	275					280				285					
Glu	Ser	Asn	Val	Leu	Val	Leu	Val	Gln	Tyr	Pro	Asp	Arg	Ser	Lys	Leu
	290				295					300					
Tyr	Thr	Gly	Asn	Pro	Ile	Thr	Ile	Lys	Ser	Val	Ser	Asp	Lys	Asn	Pro
305				310						315					320
Tyr	Ser	Arg	Ile	Leu	Asn	Gly	Asp	Asn	Ile	Ile	Leu	His	Met	Leu	Tyr
			325					330					335		
Asn	Ser	Arg	Lys	Tyr	Met	Ile	Ile	Arg	Asp	Thr	Asp	Thr	Ile	Tyr	Ala
		340						345					350		
Thr	Gln	Gly	Gly	Asp	Cys	Ser	Gln	Asn	Cys	Val	Tyr	Ala	Leu	Lys	Leu
	355					360						365			
Gln	Ser	Asn	Leu	Gly	Asn	Tyr	Gly	Ile	Gly	Ile	Phe	Ser	Ile	Lys	Asn
	370				375					380					
Ile	Val	Ser	Lys	Asn	Lys	Tyr	Cys	Ser	Gln	Ile	Phe	Ser	Ser	Phe	Arg
385				390						395					400
Glu	Asn	Thr	Met	Leu	Leu	Ala	Asp	Ile	Tyr	Lys	Pro	Trp	Arg	Phe	Ser
			405					410					415		
Phe	Lys	Asn	Ala	Tyr	Thr	Pro	Val	Ala	Val	Thr	Asn	Tyr	Glu	Thr	Lys
		420						425				430			
Leu	Leu	Ser	Thr	Ser	Ser	Phe	Trp	Lys	Phe	Ile	Ser	Arg	Asp	Pro	Gly
	435						440					445			
Trp	Val	Glu													
	450														

<210> 13
 <211> 1400
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTE Hc

<400> 13

gaattcacca	tgggagagag	tcagcaagaa	ctaaattcta	tggttaactga	taccctaaat	60
aatagtatct	cttttaagct	ttcttcttat	acagatgata	aaattttaat	ttcctacttc	120
aacaagttct	tcaagagaat	taagtcttct	tccgttttaa	acatgagata	caagaatgat	180
aaatacgtcg	acacttccgg	ttacgactcc	aatatcaaca	ttaacggtga	cgtgtacaag	240
tacccaacta	acaaaaacca	attcgggtatc	tacaacgaca	agcttactga	gctgaacatc	300
tctcaaaacg	actacattat	ctacgacaac	aagtacaaga	acttctctat	ttctttctgg	360
gtcaggattc	ctaactacga	caacaagatc	gtcaacgtta	acaacgagta	cactatcatc	420
aactgtatga	gagacaacaa	ctccgggttg	aaggtctctc	ttaaccacaa	cgagatcatt	480
tggaccttgc	aagacaacgc	aggtattaac	caaaagttag	cattcaacta	cggtaacgca	540
aacggtattt	ctgactacat	caacaagtgg	attttcgtca	ctatcactaa	cgacagatta	600
ggtgactcta	agctttacat	taacggtaac	ttaatcgacc	aaaagtccat	tttaaactta	660
ggtaacattc	acgtttctga	caacatctta	ttcaagatcg	ttaactgcag	ttacaccaga	720
tacattggca	ttagatactt	caacattttc	gacaaggagt	tagacgagac	cgagattcaa	780
actttatata	gcaacgaacc	taacaccaat	attttgaagg	acttctgggg	taactacttg	840
ctttacgaca	aggaatacta	cttattaaac	gtgttaaagc	caaacaactt	cattgatagg	900
agaaaggatt	ctactttaag	cattaacaac	atcagaagca	ctattctttt	agctaacaga	960
ttatactctg	gtatcaaggt	taagatccaa	agagttaaca	actcttctac	taacgataac	1020

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cttgtagaa agaacgatca ggtctatatt aacttcgctg ctagcaagac tcacttattc 1080
ccattatatg ctgataccgc taccaccaac aaggagaaga ccatcaagat ctctctctct 1140
ggcaacagat ttaaccaagt cgtcggtatg aactccgctg gtaacaactg taccatgaac 1200
tttaaaaata ataatggaaa taatattggg ttgtaggtt tcaaggcaga tactgtagtt 1260
gctagtactt ggtattatac ccacatgaga gatcacacca acagcaatgg atgttttttg 1320
aactttattt ctgaagaaca tggatggcaa gaaaaataat agggatccgc ggccgcacgc 1380
gtcccgggac tagtgaattc                                     1400

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<210> 14

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTE Hc

<400> 14

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Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu
 1          5          10          15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
 20          25          30
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
 35          40          45
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
 50          55          60
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
 65          70          75          80
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu Leu Asn
 85          90          95
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
100          105          110
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
115          120          125
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
130          135          140
Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
145          150          155          160
Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
165          170          175
Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
180          185          190
Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
195          200          205
Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
210          215          220
Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
225          230          235          240
Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
245          250          255
Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
260          265          270
Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
275          280          285
Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
290          295          300
Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser

```

305		310		315		320
Gly Ile Lys Val	Lys Ile Gln Arg Val	Asn Asn Ser Ser Thr	Asn Asp			
	325	330	335			
Asn Leu Val Arg	Lys Asn Asp Gln Val	Tyr Ile Asn Phe Val	Ala Ser			
	340	345	350			
Lys Thr His Leu	Phe Pro Leu Tyr	Ala Asp Thr Ala	Thr Thr Asn Lys			
	355	360	365			
Glu Lys Thr Ile	Lys Ile Ser Ser Ser	Gly Asn Arg Phe	Asn Gln Val			
	370	375	380			
Val Val Met Asn	Ser Val Gly Asn Asn	Cys Thr Met Asn	Phe Lys Asn			
385	390	395	400			
Asn Asn Gly Asn	Asn Ile Gly Leu Leu	Gly Phe Lys Ala	Asp Thr Val			
	405	410	415			
Val Ala Ser Thr	Trp Tyr Tyr Thr	His Met Arg Asp	His Thr Asn Ser			
	420	425	430			
Asn Gly Cys Phe	Trp Asn Phe Ile	Ser Glu Glu His	Gly Trp Gln Glu			
	435	440	445			
Lys						

<210> 15
 <211> 1317
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hc

<400> 15

gaattcacga	tgtcctacac	caacgacaag	atcctgatct	tgtacttcaa	caagctgtac	60
aagaagatca	aggacaactc	catcttggac	atgagatacg	aaaacaataa	gttcatcgac	120
atctccggtt	acggttccaa	catctccatc	aacgggtgacg	tctacatcta	ctccaccaat	180
agaaaccagt	tcggaatcta	ctcctccaag	ccttccgagg	tcaacatcgc	tcagaacaac	240
gacatcatct	acaacggaag	ataccagaac	ttctccatct	ccttctgggt	ccgtatccca	300
aagtacttca	acaaggtcaa	cctgaataac	gagtacacca	tcacgcgactg	catccgtaac	360
aataactccg	gatggaagat	ctccctgaac	tacaacaaga	tcacatggac	cctgcaggac	420
accgccggta	acaatcagaa	gttgggtctt	aactacaccc	agatgatctc	catctccgac	480
tacatcaaca	agtggatctt	cgtcaccatc	accaataacc	gtttgggaaa	ctccagaatc	540
tacatcaacg	gtaacttgat	cgacgagaag	tccatctcca	acttgggtga	catccacgtc	600
tccgacaaca	ttttgttcaa	gatcgtcggt	tgtaacgaca	cccgttacgt	cgggatccgt	660
tacttcaaag	tcttcgacac	tgagttgggt	aagaccgaga	tcgagacctt	gtactccgac	720
gagcctgacc	catccatcct	gaaggacttc	tggggtaact	acctgctgta	caacaaacgt	780
tactacttgc	tgaacttggt	gcgtaccgac	aagtccatca	cccagaactc	caacttcttg	840
aacatcaacc	agcagagagg	tgtctaccag	aagccaaaca	tcttctccaa	caccagattg	900
tacaccggag	tcgaggtcat	tatcagaaag	aacggatcta	ctgatatttc	caacaccgat	960
aacttcgtca	gaaagaacga	tctggcttac	atcaacgttg	tcgacagaga	tgtcgaatac	1020
cgtctgtacg	ccgatatact	tatcgccaaa	cctgaaaaga	tcacaaagct	gatccgtacc	1080
tctaactcta	acaactctct	gggacaaatc	atcgtcatgg	actccatcgg	taataactgt	1140
accatgaact	tccagaacaa	caacggtgga	aacatcggtt	tggtgggttt	ccactccaac	1200
aacttggtcg	cttctctctg	gtactacaac	aacatccgta	agaacacctc	ctccaacggt	1260
tgcttctggt	ccttcatctc	caaggagcac	ggttggcagg	agaactaata	ggaattc	1317

<210> 16
 <211> 432
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 16

Met	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu
1				5				10					15		
Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn
			20					25				30			
Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn
		35					40				45				
Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55				60					
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70				75					80	
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
			85					90					95		
Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105				110			
Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
		115					120				125				
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135				140					
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150				155					160	
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165					170					175		
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
			180					185				190			
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
		195					200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230				235					240	
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245					250					255		
Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln
			260					265				270			
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
	275						280					285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305				310					315					320	
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325					330					335		
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
		340						345				350			
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
		355				360					365				
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
	370				375					380					
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385				390					395					400	
Ala	Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn

	405		410		415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn					
	420		425		430

<210> 17
 <211> 1368
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTG Hc

<400> 17
 gaattcacga tgaaggacac catcctgata cagggtcttca acaactacat ctccaacatc 60
 tcttccaacg ccatcctgtc cctgtcctac cgtgggtggc gtctgatcga ctctccgggt 120
 tacggagcca ccatgaacgt cggttccgac gtcattcttca acgacatcgg taacgggtcag 180
 ttcaagctga acaactccga gaactccaac atcacgcgcc accagtccaa gttcgtcgtc 240
 tacgactcca tgttcgacaa cttctccatc aacttctggg tccgtacccc aaagtacaac 300
 aacaacgaca tccagacctt cctgcagaac gactacacca tcatctcctg tatcaagaac 360
 gactccgggtt ggaaggtctc catcaaggga aaccgtatca tctggaccct gatcgacgtc 420
 aacgccaagt ccaagtccat cttcttcgag tactccatca aggacaacat ctccgactac 480
 atcaacaagt ggttctccat caccatcacc aacgaccgtc tgggtaacgc caacatctac 540
 atcaacgggt cctgaagaa gtccgagaag atcctgaacc tggaccgtat caactcctcc 600
 aacgacatcg acttcaagct gatcaactgt accgacacca ccaagttcgt ctggatcaag 660
 gacttcaaca tcttcgggtc tgagctgaac gccaccgagg tctcctccct gtactggatc 720
 cagtcttcca ccaacaccct gaaggacttc tggggaaacc cactgcgtta cgacacccag 780
 tactacctgt tcaaccaggg tatgcagaac atctacatca agtacttctc caaggcctcc 840
 atgggtgaga ccgccccctc taccaacttc aacaacgccc ccatcaacta ccagaacctg 900
 tacctgggtc tgcgtttcat catcaagaag gcctccaact cccgtaacat caacaacgac 960
 aacatcgctc gtgagggtga ctacatctac ctgaacatcg acaacatctc cgacgagtcc 1020
 taccgtgtct acgtcctggt caactccaag gagatccaga cccagctggt cctggcccca 1080
 atcaacgacg accctacctt ctacgacgtc ctgcagatca agaagtacta cgagaagacc 1140
 acctacaact gtcagatcct gtgcgagaag gacaccaaga ccttcggact gttcgggtatc 1200
 ggtaagttcg tcaaggacta cggttacgtc tgggacacct acgacaacta cttctgtatc 1260
 tcccagtggt acctgcgtcg tatctccgag aacatcaaca agctgcgtct gggatgtaac 1320
 tggcagttca tcccagtcga cgagggttgg accgagtaat aggaattc 1368

<210> 18
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTG Hc

<400> 18
 Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
 1 5 10 15
 Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
 20 25 30
 Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
 35 40 45
 Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
 50 55 60
 Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser

65					70					75				80
Met	Phe	Asp	Asn	Phe	Ser	Ile	Asn	Phe	Trp	Val	Arg	Thr	Pro	Lys Tyr
				85					90					95
Asn	Asn	Asn	Asp	Ile	Gln	Thr	Tyr	Leu	Gln	Asn	Glu	Tyr	Thr	Ile Ile
			100					105					110	
Ser	Cys	Ile	Lys	Asn	Asp	Ser	Gly	Trp	Lys	Val	Ser	Ile	Lys	Gly Asn
			115				120					125		
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Val	Asn	Ala	Lys	Ser	Lys	Ser Ile
	130					135				140				
Phe	Phe	Glu	Tyr	Ser	Ile	Lys	Asp	Asn	Ile	Ser	Asp	Tyr	Ile	Asn Lys
145					150					155				160
Trp	Phe	Ser	Ile	Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asn	Ala	Asn Ile
				165					170					175
Tyr	Ile	Asn	Gly	Ser	Leu	Lys	Lys	Ser	Glu	Lys	Ile	Leu	Asn	Leu Asp
			180					185					190	
Arg	Ile	Asn	Ser	Ser	Asn	Asp	Ile	Asp	Phe	Lys	Leu	Ile	Asn	Cys Thr
		195					200						205	
Asp	Thr	Thr	Lys	Phe	Val	Trp	Ile	Lys	Asp	Phe	Asn	Ile	Phe	Gly Arg
	210					215					220			
Glu	Leu	Asn	Ala	Thr	Glu	Val	Ser	Ser	Leu	Tyr	Trp	Ile	Gln	Ser Ser
225					230					235				240
Thr	Asn	Thr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Arg	Tyr	Asp Thr
				245					250					255
Gln	Tyr	Tyr	Leu	Phe	Asn	Gln	Gly	Met	Gln	Asn	Ile	Tyr	Ile	Lys Tyr
			260					265					270	
Phe	Ser	Lys	Ala	Ser	Met	Gly	Glu	Thr	Ala	Pro	Arg	Thr	Asn	Phe Asn
		275					280					285		
Asn	Ala	Ala	Ile	Asn	Tyr	Gln	Asn	Leu	Tyr	Leu	Gly	Leu	Arg	Phe Ile
	290					295					300			
Ile	Lys	Lys	Ala	Ser	Asn	Ser	Arg	Asn	Ile	Asn	Asn	Asp	Asn	Ile Val
305					310					315				320
Arg	Glu	Gly	Asp	Tyr	Ile	Tyr	Leu	Asn	Ile	Asp	Asn	Ile	Ser	Asp Glu
				325					330					335
Ser	Tyr	Arg	Val	Tyr	Val	Leu	Val	Asn	Ser	Lys	Glu	Ile	Gln	Thr Gln
			340					345					350	
Leu	Phe	Leu	Ala	Pro	Ile	Asn	Asp	Asp	Pro	Thr	Phe	Tyr	Asp	Val Leu
		355					360					365		
Gln	Ile	Lys	Lys	Tyr	Tyr	Glu	Lys	Thr	Thr	Tyr	Asn	Cys	Gln	Ile Leu
	370					375					380			
Cys	Glu	Lys	Asp	Thr	Lys	Thr	Phe	Gly	Leu	Phe	Gly	Ile	Gly	Lys Phe
385					390				395					400
Val	Lys	Asp	Tyr	Gly	Tyr	Val	Trp	Asp	Thr	Tyr	Asp	Asn	Tyr	Phe Cys
				405					410				415	
Ile	Ser	Gln	Trp	Tyr	Leu	Arg	Arg	Ile	Ser	Glu	Asn	Ile	Asn	Lys Leu
			420					425					430	
Arg	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Val	Asp	Glu	Gly	Trp Thr
		435					440					445		
Glu														

<210> 19
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Synthetic construct based on BoNTA Hn

<400> 19

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atggctctga acgacctgtg catcaaagtt aacaactggg acctgttctt ctccccgtct 60
gaagacaact tcactaacga cctgaacaaa ggcgagaaga tcacctccga cactaacatc 120
gaagctgctg aagaaaacat ctctctggac ctgatccagc agtactacct gactttcaac 180
ttcgacaacg aaccggaaaa catctccatc gaaaacctgt cttccgacat catcggtcag 240
ctggaactga tgccgaacat cgaacgcttc ccgaacggca agaaatacga actggacaaa 300
tacaccatgt tccactacct gcgtgctcag gaattcgaac acggtaaata tcgtatcgct 360
ctgactaact ccgttaacga agctctgctg aacctgtctc gcgtttacac cttcttctct 420
tccgactacg ttaagaaagt taacaaagct actgaagctg ctatgttcct gggttggggt 480
gaacagctgg tttacgactt caccgacgaa acttctgaag tttccaccac tgacaaaatc 540
gctgacatca ctatcatcat cccgtacatc ggcccggctc tgaacatcgg taacatgctg 600
tacaagacg acttcggttg tgctctgata ttctctggcg ctgttatcct gctggaattc 660
atcccggaag tcgctatccc ggttctgggt accttcgctc tggtttccta catcgctaac 720
aaagttctga ctgttcagac catcgacaaac gctctgtcta aacgtaacga aaaatgggac 780
gaagttttaca aatacatcgt tactaactgg ctggctaaag ttaacactca gatcgacctg 840
atccgtaaga agatgaaaga agctctggaa aaccaggctg aagctactaa agctatcatc 900
aactaccagt acaaccagta caccgaagaa gaaaagaaca acatcaactt caacatcgat 960
gacctgtcct ctaaactgaa cgaatccatc aacaaagcta tgatcaacat caacaaattc 1020
ctgaaccagt gctctgtttc ctacctgatg aactctatga tcccgtagcg cgttaaacgc 1080
ctggaagact tcgacgcttc cctgaaagac gctctgctga aatacatccg tgacaactac 1140
gggtactctga tcggccaggt tgaccgtctg aaagacaagg ttaacaacac cctgtctact 1200
gacatcccgt tccagctgtc caaatacgtt gacaaccagt aa 1242
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<210> 20

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTA Hn

<400> 20

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Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1           5           10           15
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
          20           25           30
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
          35           40           45
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
          50           55           60
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65           70           75           80
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
          85           90           95
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
          100          105          110
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
          115          120          125
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
          130          135          140
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145          150          155          160
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
          165          170          175
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Thr	Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro
			180					185					190		
Ala	Leu	Asn	Ile	Gly	Asn	Met	Leu	Tyr	Lys	Asp	Asp	Phe	Val	Gly	Ala
		195					200					205			
Leu	Ile	Phe	Ser	Gly	Ala	Val	Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Ile
	210					215					220				
Ala	Ile	Pro	Val	Leu	Gly	Thr	Phe	Ala	Leu	Val	Ser	Tyr	Ile	Ala	Asn
225					230					235					240
Lys	Val	Leu	Thr	Val	Gln	Thr	Ile	Asp	Asn	Ala	Leu	Ser	Lys	Arg	Asn
				245					250						255
Glu	Lys	Trp	Asp	Glu	Val	Tyr	Lys	Tyr	Ile	Val	Thr	Asn	Trp	Leu	Ala
		260						265					270		
Lys	Val	Asn	Thr	Gln	Ile	Asp	Leu	Ile	Arg	Lys	Lys	Met	Lys	Glu	Ala
	275						280					285			
Leu	Glu	Asn	Gln	Ala	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asn	Tyr	Gln	Tyr
	290					295					300				
Asn	Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp
305					310					315					320
Asp	Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn
				325					330					335	
Ile	Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser
			340					345					350		
Met	Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu
	355					360					365				
Lys	Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Arg	Asp	Asn	Tyr	Gly	Thr	Leu	Ile
	370					375					380				
Gly	Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr
385					390					395					400
Asp	Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln			
			405					410							

<210> 21
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTB Hn

<400> 21
 atggctccag gaatctgtat cgacgtcgac aacgaggact tggtcttcat cgctgacaag 60
 aactccttct ccgacgactt gtccaagaac gagagaatcg agtacaacac ccagtccaac 120
 tacatcgaga acgacttccc aatcaacgag ttgatcttgg acaccgactt gatctccaag 180
 atcgagttgc catccgagaa caccgagtc ttgactgact tcaacgtcga cgtcccagtc 240
 tacgagaagc aaccagctat caagaagatt ttcaccgacg agaacacccat cttccaatac 300
 ctgtactctc agaccttccc tttggacatc agagacatct ccttgacctc ttccttcgac 360
 gacgccttgc tggtctccaa caaggtctac tccttcttct ccatggacta catcaagact 420
 gctaacaagg tcgtcgaggg cggtttgttc gctggttggg tcaagcagat cgtcaacgat 480
 ttogtcatcg aggctaaca gtccaacacc atggacaaga ttgccgacat ctcccttgatt 540
 gtcccataca tcggtttggc cttgaacgtc ggtaacgaga cgcgaaggg taacttcgag 600
 aacgctttcg agatcgctgg tgcctccatc ttgttggagt tcatcccaga gttgttgatc 660
 ccagtcgtcg gtgccttctt gttggagtc tacatcgaca acaagaacaa gatcatcaag 720
 accatcgaca acgctttgac caagagaaac gagaagtggc ccgacatgta cggtttgatc 780
 gtcgcccatt ggttgtccac cgtcaacacc caattctaca ccatcaagga gggatatgtac 840
 aaggccttga actaccaggc ccaagctttg gaggagatca tcaagtacag atacaacatc 900
 tactccgaga aggagaagtc caacattaac atcgacttca acgacatcaa ctccaagctg 960

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aacgagggtta ttaaccaggc catcgacaac atcaacaact tcatcaacgg ttgttccgtc 1020
tcctacttga tgaagaagat gattccattg gccgtcgaga agttgttgga cttcgacaac 1080
accctgaaga agaacttggt gaactacatc gacgagaaca agttgtactt gatcggttcc 1140
gctgagtacg agaagtccaa ggtcaacaag tacttgaaga ccatcatgcc attcgacttg 1200
tccatctaca ccaacgacac catcttgatc gagatgttct aa 1242

```

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<210> 22
<211> 413
<212> PRT
<213> Artificial Sequence

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<220>
<223> Encoded polypeptide of a synthetic construct based
      on BoNTB Hn

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```

<400> 22
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
 1           5           10           15
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
      20           25           30
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
      35           40           45
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
      50           55           60
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
      65           70           75           80
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
      85           90           95
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
      100          105          110
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
      115          120          125
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
      130          135          140
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
      145          150          155          160
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
      165          170          175
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
      180          185          190
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
      195          200          205
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
      210          215          220
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
      225          230          235          240
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
      245          250          255
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
      260          265          270
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
      275          280          285
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
      290          295          300
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
      305          310          315          320
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn

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				325					330					335					
Gly	Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val				
				340				345						350					
Glu	Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn				
				355				360						365					
Tyr	Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu				
				370				375						380					
Lys	Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu				
						390					395				400				
Ser	Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe							
				405						410									

<210> 23
 <211> 1200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTC1 Hn

<400> 23
 atgtccctgt acaacaagac ccttgactgt agagagctgc tgggtgaagaa cactgacctg 60
 ccattcatcg gtgacatcag tgacgtgaag actgacatct tcctgcgtaa ggacatcaac 120
 gaggagactg aggtgatcta ctaccagac aacgtgtcag tagaccaagt gatcctcagt 180
 aagaacacct ccgagcatgg acaactagac ctgctctacc ctagtatcga cagtggagagt 240
 gagatcctgc caggggagaa tcaagtcttc tacgacaacc gtaccagaa cgtggactac 300
 ctgaactcct actactacct agagtctcag aagctgagtg acaacgtgga ggacttcaact 360
 ttcaacgcgtt caatcgagga ggctctggac aacagtgcaa aggtgtacac ttacttccct 420
 accctggcta acaaggtgaa tgccgggtgtg caaggtggtc tgttctgat gtgggcaaac 480
 gacgtgggtg aggacttcac taccaacatc ctgcgtaagg acacactgga caagatctca 540
 gatgtgtcag ctatcatccc ctacatcgga ccgcactga acatctccaa ctctgtgcgt 600
 cgtggaaact tcaactgaggc attcgcagtc actggtgtca ccatcctgct ggaggcattc 660
 cctgagttca caatccctgc tctgggtgca ttcgtgatct acagtaaggc ccaggagcga 720
 aacgagatca tcaagaccat cgacaactgt ctggagcaga ggatcaagag atggaaggac 780
 tcttacgagt ggatgatggg aacgtgggtg tccaggatca tcaccagtt caacaacatc 840
 tctaccaga tgtacgactc cctgaactac caggcaggtg caatcaaggc taagatcgac 900
 ctggagtaca agaagtactc cggaagcgac aaggagaaca tcaagagcca ggttgagaac 960
 ctgaagaaca gtctggacgt caagatctcg gaggcaatga acaacatcaa caagttcatc 1020
 cgagagtgtc ccgtcaccta cctgttcaag aacatgctgc ctaaggatcat cgacgagctg 1080
 aacgagttcg accgaaacac caaggcaaag ctgatcaacc tgatcgactc ccataacatc 1140
 atcctgggtc gtgaggtcga caagctgaag gcaaaggtaa acaacagctt ccagaactaa 1200

<210> 24
 <211> 399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTC Hn

<400> 24
 Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1 5 10 15
 Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp

			20					25					30				
Ile	Phe	Leu	Arg	Lys	Asp	Ile	Asn	Glu	Glu	Thr	Glu	Val	Ile	Tyr	Tyr		
		35					40					45					
Pro	Asp	Asn	Val	Ser	Val	Asp	Gln	Val	Ile	Leu	Ser	Lys	Asn	Thr	Ser		
	50					55					60						
Glu	His	Gly	Gln	Leu	Asp	Leu	Leu	Tyr	Pro	Ser	Ile	Asp	Ser	Glu	Ser		
65					70					75					80		
Glu	Ile	Leu	Pro	Gly	Glu	Asn	Gln	Val	Phe	Tyr	Asp	Asn	Arg	Thr	Gln		
			85						90					95			
Asn	Val	Asp	Tyr	Leu	Asn	Ser	Tyr	Tyr	Tyr	Leu	Glu	Ser	Gln	Lys	Leu		
		100					105						110				
Ser	Asp	Asn	Val	Glu	Asp	Phe	Thr	Phe	Thr	Arg	Ser	Ile	Glu	Glu	Ala		
	115						120					125					
Leu	Asp	Asn	Ser	Ala	Lys	Val	Tyr	Thr	Tyr	Phe	Pro	Thr	Leu	Ala	Asn		
	130					135					140						
Lys	Val	Asn	Ala	Gly	Val	Gln	Gly	Gly	Leu	Phe	Leu	Met	Trp	Ala	Asn		
145				150					155					160			
Asp	Val	Val	Glu	Asp	Phe	Thr	Thr	Asn	Ile	Leu	Arg	Lys	Asp	Thr	Leu		
		165					170						175				
Asp	Lys	Ile	Ser	Asp	Val	Ser	Ala	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala		
		180					185					190					
Leu	Asn	Ile	Ser	Asn	Ser	Val	Arg	Arg	Gly	Asn	Phe	Thr	Glu	Ala	Phe		
	195					200					205						
Ala	Val	Thr	Gly	Val	Thr	Ile	Leu	Leu	Glu	Ala	Phe	Pro	Glu	Phe	Thr		
	210				215					220							
Ile	Pro	Ala	Leu	Gly	Ala	Phe	Val	Ile	Tyr	Ser	Lys	Val	Gln	Glu	Arg		
225				230					235					240			
Asn	Glu	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Lys		
		245					250					255					
Arg	Trp	Lys	Asp	Ser	Tyr	Glu	Trp	Met	Gly	Thr	Trp	Leu	Ser	Arg			
	260					265					270						
Ile	Ile	Thr	Gln	Phe	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Tyr	Asp	Ser	Leu		
	275				280						285						
Asn	Tyr	Gln	Ala	Gly	Ala	Ile	Lys	Ala	Lys	Ile	Asp	Leu	Glu	Tyr	Lys		
	290				295				300								
Lys	Tyr	Ser	Gly	Ser	Asp	Lys	Glu	Asn	Ile	Lys	Ser	Gln	Val	Glu	Asn		
305				310					315					320			
Leu	Lys	Asn	Ser	Leu	Asp	Val	Lys	Ile	Ser	Glu	Ala	Met	Asn	Asn	Ile		
		325					330					335					
Asn	Lys	Phe	Ile	Arg	Glu	Cys	Ser	Val	Thr	Tyr	Leu	Phe	Lys	Asn	Met		
	340				345						350						
Leu	Pro	Lys	Val	Ile	Asp	Glu	Leu	Asn	Glu	Phe	Asp	Arg	Asn	Thr	Lys		
	355				360						365						
Ala	Lys	Leu	Ile	Asn	Leu	Ile	Asp	Ser	His	Asn	Ile	Ile	Leu	Val	Gly		
	370				375					380							
Glu	Val	Asp	Lys	Leu	Lys	Ala	Lys	Val	Asn	Asn	Ser	Phe	Gln	Asn			
385				390					395								

<210> 25

<211> 1161

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTD Hn

<400> 25

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atggccaact cccgtgacga ctccacctgc atcaagggtca agaacaacag actgccatac 60
gttgccgaca aggactccat ctcccaggag atcttcgaga acaagatcat caccgacgag 120
accaacgttc aaaactactc cgacaagttc tctttggacg agtccatcct ggacgggtcag 180
gtcccaatca acccagagat cgtcgaccca ctggttgcaa acgtcaacat ggagccattg 240
aacttgccag gtgaggagat cgtcttctac gacgacatca ccaagtacgt cgactacttg 300
aactcctact actacttggg gtctcaaaag ttgtctaaca acgtcgagaa catcaccttg 360
accacctccg tcgaggaggc cttgggttac tctaacaaga tctacacctt cctgccatcc 420
ttggctgaga aggttaacaa ggggtgtcaa gctggtttgt tctgaactg ggccaacgag 480
gtcgtcgagg acttcaccac caacatcatg aagaaggaca ccctggacaa gatctccgac 540
gtctccgtca tcatcccata catcgggtcca gccttgaaca tcggtaactc cgccctgaga 600
ggtaacttca accaggcctt cgccaccgcc ggtgtgcctt tctgtctgga gggtttccca 660
gagttcacca tcccagccct ggggtgtctt acccttctact cctccatcca ggagagagag 720
aagatcatca agaccatcga gaactgcttg gagcagagag tcaagagatg gaaggactcc 780
taccagtggg tggtttccaa ctggctgtcc agaatcacca cccaattcaa ccacatcaac 840
taccagatgt acgactccct gtccctaccg gccgacgcca tcaaggccaa gatcgacctg 900
gagtacaaga agtactccgg ttccgacaag gagaacatca agtcccaggt cgagaacctg 960
aagaactcct tggacgtcaa gatctccgag gccatgaaca acatcaacaa gttcatccgt 1020
gagtgttccg tcacctacct gttcaagaac atgctgccaa aggtcatcga cgagctgaac 1080
aagttcgacc tgagaaccaa gaccgagctg atcaacctga tcgactccca caacatcatc 1140
ctggttgggt aggttgacta a                                     1161
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<210> 26

<211> 386

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTD Hn

<400> 26

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Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1           5           10          15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
 20          25          30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
 35          40          45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
 50          55          60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
 65          70          75          80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
 85          90          95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
100         105         110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
115         120         125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
130         135         140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145         150         155         160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
165         170         175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
180         185         190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
```

	195		200		205	
Thr	Ala Gly Val	Ala Phe Leu	Leu Glu Gly Phe	Pro Glu Phe Thr	Ile	
	210		215		220	
Pro	Ala Leu Gly Val	Phe Thr Phe Tyr Ser	Ser Ile Gln Glu Arg	Glu		
225		230		235		240
Lys	Ile Ile Lys Thr	Ile Glu Asn Cys	Leu Glu Gln Arg	Val Lys Arg		
	245		250		255	
Trp	Lys Asp Ser Tyr	Gln Trp Met Val	Ser Asn Trp Leu	Ser Arg Ile		
	260		265		270	
Thr	Thr Gln Phe Asn	His Ile Asn Tyr	Gln Met Tyr Asp	Ser Leu Ser		
	275		280		285	
Tyr	Gln Ala Asp Ala	Ile Lys Ala Lys	Ile Asp Leu Glu	Tyr Lys Lys		
	290		295		300	
Tyr	Ser Gly Ser Asp	Lys Glu Asn Ile	Lys Ser Gln Val	Glu Asn Leu		
305		310		315		320
Lys	Asn Ser Leu Asp	Val Lys Ile Ser	Glu Ala Met Asn	Asn Ile Asn		
	325		330		335	
Lys	Phe Ile Arg Glu	Cys Ser Val Thr	Tyr Leu Phe Lys	Asn Met Leu		
	340		345		350	
Pro	Lys Val Ile Asp	Glu Leu Asn Lys	Phe Asp Leu Arg	Thr Lys Thr		
	355		360		365	
Glu	Leu Ile Asn Leu	Ile Asp Ser His	Asn Ile Ile Leu	Val Gly Glu		
	370		375		380	
Val Asp						
385						

<210> 27

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct based on BoNTE Hn

<400> 27

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atgtccatct gcatcgagat caacaacggt gagctgttct tcgtggcttc cgagaacagt 60
tacaacgatg acaacatcaa cactcctaag gagattgacg acaccgtcac ttctaacaac 120
aactacgaaa acgacctgga ccagggtcatc cttaaacttca actccgagtc cgcccctggt 180
ctgtccgacg agaagctgaa cctgaccatc cagaacgacg cttacatccc aaagtacgac 240
tccaacggta catccgatat cgagcagcat gacgttaacg agcttaacgt cttctttctac 300
ttagacgctc agaaggtgcc cgaggggtgag aacaacgtca atctcacctc ttcaattgac 360
acagccttgt tggagcagcc taagatctac accttcttct cctccgagtt catcaacaac 420
gtcaacaagc ctgtgcaggc cgcattgttc gtaagctgga ttcagcaggt gttagtagac 480
ttcactactg aggctaacca gaagtccact gttgacaaga tcgctgacat ctccatcgtc 540
gtcccataca tcggtctggc tctgaacatc ggcaacgagg cacagaaggg caacttcaag 600
gatgcccttg agttgttggg tgccggtatt ttgttggagt tcgaaccgga gctgctgac 660
cctaccatcc tggtcttcac gatcaagtcc ttcttggtt cctccgacaa caagaacaag 720
gtcattaagg ccatcaacaa cgccctgaag gagcgtgacg agaagtggaa ggaagtctat 780
tccttcatcg tctcgaactg gatgaccaag atcaacacc agttcaacaa gcgaaaggag 840
cagatgtacc aggctctgca gaaccaggtc aacgccatca agaccatcat cgagtccaag 900
tacaactcct acaccctgga ggagaagaac gagcttacca acaagtacga tatcaagcag 960
atcgagaacg agctgaacca gaaggtctcc atcgccatga acaacatcga caggttcctg 1020
accgagtcct ccattctcta cctgatgaag ctcatcaacg aggtcaagat caacaagctg 1080
cgagagtacg acgagaatgt caagacgtac ctgctgaact acatcatcca gcacggatcc 1140
atcctgtaa                                     1149

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<210> 28
 <211> 382
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTE Hn

<400> 28
 Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1 5 10 15
 Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
 20 25 30
 Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
 35 40 45
 Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
 50 55 60
 Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
 65 70 75 80
 Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
 85 90 95
 Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
 100 105 110
 Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
 115 120 125
 Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
 130 135 140
 Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
 145 150 155 160
 Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
 165 170 175
 Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
 180 185 190
 Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
 195 200 205
 Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
 210 215 220
 Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
 225 230 235 240
 Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
 245 250 255
 Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
 260 265 270
 Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
 275 280 285
 Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
 290 295 300
 Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
 305 310 315 320
 Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
 325 330 335
 Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
 340 345 350
 Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
 355 360 365
 Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu

370

375

380

<210> 29
 <211> 1227
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hn

<400> 29
 atggccccac cacgtctgtg tattagagtc aacaactcag aattattctt tgctgcttcc 60
 gagtcaagct acaacgagaa cgatattaac acacctaaag agattgacga tactaccaac 120
 ctaaacaaca actaccgga caacttggat gaggttattt tggattacaa ctacagagacc 180
 atccctcaaa ttccaaccg taccttaaac actcttgtcc aagacaactc ctacgttcca 240
 agatacgatt ctaacggtac ctacagagatc gaggagtatg atgttggtga ctttaacgtc 300
 tttttctatt tgcattgccc gaaggtgcc gaaggtgaaa ccaacatctc attgacttct 360
 tccattgata cgccttgtt ggaagagtc aaggatatct tcttttcttc ggagtttctc 420
 gatactatca acaagcctgt caacgcctgt ctgttcattg attggattag caaggtcatc 480
 agagatttta cactgaagc tactcaaaag tccactgttg ataagattgc tgacatctct 540
 ttgattgtcc cctatgtcgg tcttgctttg aacatcatta ttgaggcaga aaagggtaac 600
 tttgaggagg cttttgaatt gttgggagtt ggtattttgt tggagtttgt tccagaactt 660
 accattcctg tcatttttagt ttttacgata aagtcctaca tcgattcata cgagaacaag 720
 aataaagcaa ttaaagctat taacaactcc ttgatcgaaa gagaggctaa gtggaaggaa 780
 atctactcat ggattgtatc aaactggctt actagaatta acactcaatt taacaagaga 840
 aaggagcaaa tgtaccaggc tctgcaaaac caagtcgatg ctatcaagac tgcaattgaa 900
 tacaagtaca acaactatac ttccgatgag aagaacagac ttgaatctga atacaatatc 960
 aacaacattg aagaagagtt gaacaagaaa gtttctttgg ctatgaagaa tatcgaaaga 1020
 tttatgaccg aatcctctat ctcttacttg atgaagttga tcaatgaggc caaggttggt 1080
 aagttgaaga agtacgataa ccacgttaag agcgatctgc tgaactacat tctcgaccac 1140
 agatcaatcc tgggagagca gacaaacgag ctgagtgatt tggttacttc cactttgaac 1200
 tcctccattc catttgagct ttcttaa 1227

<210> 30
 <211> 408
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Encoded polypeptide of a synthetic construct based
 on BoNTF Hn

<400> 30
 Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1 5 10 15
 Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
 20 25 30
 Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
 35 40 45
 Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
 50 55 60
 Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
 65 70 75 80
 Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
 85 90 95
 Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly


```

acaaaccttg ttgaaaaagc taatacagtt gtaggtgctt cactttttgt aaactgggta 480
aaaggagtaa tagatgattt tacatctgaa tccacacaaa aaagtactat agataaagtt 540
tcagatgtat ccataattat tccctatata ggacctgctt tgaatgtagg aaatgaaaca 600
gctaaagaaa attttaaaaa tgcttttgaa ataggtggag ccgctatctt aatggagttt 660
attccagaac ttattgtacc tatagttgga ttttttacat tagaatcata tgtaggaaat 720
aaagggcata ttattatgac gatatccaat gctttaaaga aaagggatca aaaatggaca 780
gatatgtatg gtttgatagt atcgcagtggt ctctcaacgg ttaatactca attttataca 840
ataaaagaaa gaatgtacaa tgctttaaat aatcaatcac aagcaataga aaaaataata 900
gaagatcaat ataatagata tagtgaagaa gataaaatga atattaacat tgattttaat 960
gatatagatt ttaaacttaa tcaaagtata aatttagcaa taaacaatat agatgatttt 1020
ataaaccaat gttctatata atattctaag aatagaatga ttccattagc tgtaaaaaag 1080
ttaaaagact ttgatgataa tcttaagaga gattttattgg agtatataga tacaaatgaa 1140
ctatatattac ttgatgaagt aaatattcta aaatcaaaag taaatagaca cctaaaagac 1200
agtataccat ttgatctttc actatatacc taa                                     1233

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<210> 32

<211> 410

<212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTG Hn

<400> 32

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Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
1           5           10           15
Glu Asp Leu Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
20           25           30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
35           40           45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
50           55           60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65           70           75           80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
85           90           95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
100          105          110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
115          120          125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
130          135          140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145          150          155          160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
165          170          175
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
180          185          190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
195          200          205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
210          215          220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225          230          235          240
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
245          250          255

```

Gln	Lys	Trp	Thr	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ser	Gln	Trp	Leu	Ser
			260					265					270		
Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Arg	Met	Tyr	Asn	Ala
		275					280					285			
Leu	Asn	Asn	Gln	Ser	Gln	Ala	Ile	Glu	Lys	Ile	Ile	Glu	Asp	Gln	Tyr
	290				295						300				
Asn	Arg	Tyr	Ser	Glu	Glu	Asp	Lys	Met	Asn	Ile	Asn	Ile	Asp	Phe	Asn
305					310					315				320	
Asp	Ile	Asp	Phe	Lys	Leu	Asn	Gln	Ser	Ile	Asn	Leu	Ala	Ile	Asn	Asn
			325					330						335	
Ile	Asp	Asp	Phe	Ile	Asn	Gln	Cys	Ser	Ile	Ser	Tyr	Leu	Met	Asn	Arg
			340					345					350		
Met	Ile	Pro	Leu	Ala	Val	Lys	Lys	Leu	Lys	Asp	Phe	Asp	Asp	Asn	Leu
		355					360					365			
Lys	Arg	Asp	Leu	Leu	Glu	Tyr	Ile	Asp	Thr	Asn	Glu	Leu	Tyr	Leu	Leu
	370					375					380				
Asp	Glu	Val	Asn	Ile	Leu	Lys	Ser	Lys	Val	Asn	Arg	His	Leu	Lys	Asp
385					390					395					400
Ser	Ile	Pro	Phe	Asp	Leu	Ser	Leu	Tyr	Thr						
			405					410							

<210> 33
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTF Hc

<400> 33
 gaattcacga tgtcttacac taacgacaaa atcctgatcc tgtacttcaa caaactgtac 60
 aaaaaaatca aagacaactc tatcctggac atgcggttacg aaaacaacaa attcatcgac 120
 atctctggct atggttctaa catctctatc aacggtgacg tctacatcta ctctactaac 180
 cgcaaccagt tcggtatcta ctcttctaaa ccgtctgaag taaacatcgc tcagaacaac 240
 gacatcatct acaacggctc ttaccagaac ttctctatct ctttctgggt tcgtatcccg 300
 aaatacttca acaaagttaa cctgaacaac gaatacacta tcatcgactg catccgtaac 360
 aacaactctg gttggaaaat ctctctgaac tacaacaaaa tcatctggac tctgcaggac 420
 actgctggta acaaccagaa actgggtttc aactacactc agatgatctc tatctctgac 480
 tacattaata aatggatctt cgttactatc actaacaacc gtctgggtaa ctctcgtatc 540
 tacatcaacg gtaacctgat cgatgaaaaa tctatctcta acctgggtga catccacggt 600
 tctgacaaca tcctgttcaa aatcggttgg tgcaacgaca cgcgttacgt tggatccggt 660
 tacttcaaag ttttcgacac tgaactgggt aaaactgaaa tcgaaactct gtactctgac 720
 gaaccggacc cgtctatcct gaaagacttc tggggtaact acctgctgta caacaaacgt 780
 tactacctgc tgaacctgct ccggactgac aaatctatca ctacagaactc taacttctctg 840
 aacatcaacc agcagcgttg tgtttatcag aaacctaata tcttctctaa cactcgtctg 900
 tacactgggtg ttgaagttat catccgtaaa aacggttcta ctgacatctc taacactgac 960
 aacttcgtac gtaaaaacga cctgggttac atcaacgttg ttgaccgtga cggtgaatac 1020
 cgtctgtacg ctgacatctc tatcgctaaa ccggaacaaa tcatcaaact gatccgtact 1080
 tctaactcta acaactctct gggtcagatc atcggtatgg actcgatcgg taacaactgc 1140
 actatgaact tccagaacaa caacggtggt aacatcggtc tgctgggttt ccactctaac 1200
 aacctggttg cttcttcatg gtactacaac aacatccgta aaaacacttc ttctaacggt 1260
 tgcttctggt ctttcatctc taaagaacac gggtggcagg aaaactaaga attc 1314

<210> 34
 <211> 432
 <212> PRT

<213> Artificial Sequence

<220>

<223> Encoded polypeptide of a synthetic construct based
on BoNTF Hc

<400> 34

Met	Ser	Tyr	Thr	Asn	Asp	Lys	Ile	Leu	Ile	Leu	Tyr	Phe	Asn	Lys	Leu
1				5				10					15		
Tyr	Lys	Lys	Ile	Lys	Asp	Asn	Ser	Ile	Leu	Asp	Met	Arg	Tyr	Glu	Asn
			20					25				30			
Asn	Lys	Phe	Ile	Asp	Ile	Ser	Gly	Tyr	Gly	Ser	Asn	Ile	Ser	Ile	Asn
		35					40				45				
Gly	Asp	Val	Tyr	Ile	Tyr	Ser	Thr	Asn	Arg	Asn	Gln	Phe	Gly	Ile	Tyr
	50					55					60				
Ser	Ser	Lys	Pro	Ser	Glu	Val	Asn	Ile	Ala	Gln	Asn	Asn	Asp	Ile	Ile
65					70				75					80	
Tyr	Asn	Gly	Arg	Tyr	Gln	Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile
			85					90					95		
Pro	Lys	Tyr	Phe	Asn	Lys	Val	Asn	Leu	Asn	Asn	Glu	Tyr	Thr	Ile	Ile
			100					105					110		
Asp	Cys	Ile	Arg	Asn	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Leu	Asn	Tyr
	115						120					125			
Asn	Lys	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Ala	Gly	Asn	Asn	Gln	Lys
	130					135					140				
Leu	Val	Phe	Asn	Tyr	Thr	Gln	Met	Ile	Ser	Ile	Ser	Asp	Tyr	Ile	Asn
145					150				155					160	
Lys	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	Gly	Asn	Ser	Arg
			165					170					175		
Ile	Tyr	Ile	Asn	Gly	Asn	Leu	Ile	Asp	Glu	Lys	Ser	Ile	Ser	Asn	Leu
			180					185					190		
Gly	Asp	Ile	His	Val	Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Gly	Cys
	195						200					205			
Asn	Asp	Thr	Arg	Tyr	Val	Gly	Ile	Arg	Tyr	Phe	Lys	Val	Phe	Asp	Thr
	210					215					220				
Glu	Leu	Gly	Lys	Thr	Glu	Ile	Glu	Thr	Leu	Tyr	Ser	Asp	Glu	Pro	Asp
225					230				235					240	
Pro	Ser	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asn	Lys
			245					250					255		
Arg	Tyr	Tyr	Leu	Leu	Asn	Leu	Leu	Arg	Thr	Asp	Lys	Ser	Ile	Thr	Gln
			260					265					270		
Asn	Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys
	275					280						285			
Pro	Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile
	290					295					300				
Ile	Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val
305				310					315					320	
Arg	Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu
			325					330					335		
Tyr	Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile
			340					345					350		
Lys	Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile
		355				360						365			
Val	Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn
	370					375					380				
Asn	Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val
385					390					395					400

Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
405 410 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
420 425 430

<210> 35
<211> 1278
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on BoNTE Hc

<400> 35
ttcgaaacga tgattttaat ttctacttc aacaagttct tcaagagaat taagtcttct 60
tccgttttaa acatgagata caagaatgat aaatacgtcg acacttccgg ttacgactcc 120
aatatcaaca ttaacggtga cgtgtacaag tacccaacta acaaaaacca attcgggtatc 180
tacaacgaca agcttactga gctgaacatc tctcaaaacg actacattat ctacgacaac 240
aagtacaata acttctctat ttctttctgg gtcagaattc ctaactacga taacaagatc 300
gtcaacgtta acaacgagta cactatcatc aactgtatga gagacaacaa ctccgggttg 360
aaggtctctc ttaaccacaa cgagatgatt tggaccttgc aagacaacgc aggtattaac 420
caaaagttag cattcaacta cggtaacgca aacgggtattt ctgactacat caacaagtgg 480
atthtcgtca ctatcactaa cgacagatta ggggactcta agctttacat taacggtaac 540
ttaatcgacc aaaagtccat tttaaactta ggtaacattc acgtttctga caacatctta 600
ttcaagatcg ttaactgcag ttacaacaga tacattggca ttagatactt caacattttc 660
gacaaggagt tagacgagac cgagattcaa actttataca gcaacgaacc taacaccaat 720
atthtgaagg acttctgggg taactacttg ctttacgaca aggaatacta cttattaaac 780
gtgttaaagc caaacaactt cattgatagg agaaaggatt ctactttaag cattaacaac 840
atcagaagca ctattctttt agctaacaga ttatactctg gtatcaagggt taagatccaa 900
agagttaaca actcttctac taacgataac ctgtttagaa agaacgatca ggtctatatt 960
aacttcgtcg ctagcaagac tcacttattc ccattatatg ctgataacgc taccaccaac 1020
aaggagaaga ccatcaagat ctctctctct ggcaacagat ttaaccaagt cgtcgttatg 1080
aacttcgtcg gtaacaactg taccatgaac tttaaaaata ataatggaaa taatattggg 1140
tgthtaggtt tcaaggcaga tactgtagtt gctagtactt ggtattatac ccacatgaga 1200
gatcacacca acagcaatgg atgtttttgg aactttattt ctgaagaaca tggatggcaa 1260
gaaaaataat agggatcc 1278

<210> 36
<211> 419
<212> PRT
<213> Artificial Sequence

<220>
<223> Encoded polypeptide of a synthetic construct based
on BoNTE Hc

<400> 36
Met Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
1 5 10 15
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
20 25 30
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
35 40 45
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Thr Glu
50 55 60
Leu Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys

65					70					75					80
Asn	Phe	Ser	Ile	Ser	Phe	Trp	Val	Arg	Ile	Pro	Asn	Tyr	Asp	Asn	Lys
				85					90					95	
Ile	Val	Asn	Val	Asn	Asn	Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Arg	Asp
		100						105					110		
Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser	Leu	Asn	His	Asn	Glu	Ile	Ile	Trp
		115					120					125			
Thr	Leu	Gln	Asp	Asn	Ala	Gly	Ile	Asn	Gln	Lys	Leu	Ala	Phe	Asn	Tyr
	130					135					140				
Gly	Asn	Ala	Asn	Gly	Ile	Ser	Asp	Tyr	Ile	Asn	Lys	Trp	Ile	Phe	Val
145					150					155					160
Thr	Ile	Thr	Asn	Asp	Arg	Leu	Gly	Asp	Ser	Lys	Leu	Tyr	Ile	Asn	Gly
			165					170						175	
Asn	Leu	Ile	Asp	Gln	Lys	Ser	Ile	Leu	Asn	Leu	Gly	Asn	Ile	His	Val
		180						185					190		
Ser	Asp	Asn	Ile	Leu	Phe	Lys	Ile	Val	Asn	Cys	Ser	Tyr	Thr	Arg	Tyr
	195						200					205			
Ile	Gly	Ile	Arg	Tyr	Phe	Asn	Ile	Phe	Asp	Lys	Glu	Leu	Asp	Glu	Thr
	210					215					220				
Glu	Ile	Gln	Thr	Leu	Tyr	Ser	Asn	Glu	Pro	Asn	Thr	Asn	Ile	Leu	Lys
225					230					235					240
Asp	Phe	Trp	Gly	Asn	Tyr	Leu	Leu	Tyr	Asp	Lys	Glu	Tyr	Tyr	Leu	Leu
			245					250						255	
Asn	Val	Leu	Lys	Pro	Asn	Asn	Phe	Ile	Asp	Arg	Arg	Lys	Asp	Ser	Thr
		260						265					270		
Leu	Ser	Ile	Asn	Asn	Ile	Arg	Ser	Thr	Ile	Leu	Leu	Ala	Asn	Arg	Leu
	275						280					285			
Tyr	Ser	Gly	Ile	Lys	Val	Lys	Ile	Gln	Arg	Val	Asn	Asn	Ser	Ser	Thr
	290					295					300				
Asn	Asp	Asn	Leu	Val	Arg	Lys	Asn	Asp	Gln	Val	Tyr	Ile	Asn	Phe	Val
305					310					315					320
Ala	Ser	Lys	Thr	His	Leu	Phe	Pro	Leu	Tyr	Ala	Asp	Thr	Ala	Thr	Thr
			325						330					335	
Asn	Lys	Glu	Lys	Thr	Ile	Lys	Ile	Ser	Ser	Ser	Gly	Asn	Arg	Phe	Asn
		340						345					350		
Gln	Val	Val	Val	Met	Asn	Ser	Val	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe
	355						360					365			
Lys	Asn	Asn	Asn	Gly	Asn	Asn	Ile	Gly	Leu	Leu	Gly	Phe	Lys	Ala	Asp
	370					375					380				
Thr	Val	Val	Ala	Ser	Thr	Trp	Tyr	Tyr	Thr	His	Met	Arg	Asp	His	Thr
385					390					395					400
Asn	Ser	Asn	Gly	Cys	Phe	Trp	Asn	Phe	Ile	Ser	Glu	Glu	His	Gly	Trp
			405						410					415	
Gln	Glu	Lys													

<210> 37
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct based on BoNTA Hc

<400> 37
 ctcgagccat ggctcgtctg ctgtctacct tcactgaata catcaagaac atcatcaata 60


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cctccatcct gaacctgcgc tacgaatcca atcacctgat cgacctgtct cgctacgctt 120
ccaaaatcaa catcggttct aaagttaact tcgatccgat cgacaagaat cagatccagc 180
tggtcaatct ggaatcttcc aaaatcgaag ttatcctgaa gaatgctatc gtatacaact 240
ctatgtacga aaactttctcc acctccttct ggatccgcat cccgaaatac ttcaactcca 300
tctctctgaa caatgaatac accatcatca actgcatgga aaacaattct gggttgaaag 360
tatctctgaa ctacggtgaa atcatctgga ctctgcagga cactcaggaa atcaaacagc 420
gtgttgattt caaatactct cagatgatca acatctctga ctacatcaat cgctggatct 480
tcgttaccat caccaacaat cgtctgaata actccaaaat ctacatcaac ggccgctctga 540
tcgaccagaa accgatctcc aatctgggta acatccacgc ttctaataac atcatgttca 600
aactggacgg ttgtcgtgac actcaccgct acatctggat caaatacttc aatctgttcg 660
acaaagaact gaacgaaaaa gaaatcaaag acctgtacga caaccagtcc aattctggta 720
tcttgaaaga cttctggggt gactacctgc agtacgacaa accgtactac atgctgaatc 780
tgtacgatcc gaacaaatac gttgacgtca acaatgtagg tatccgcggt tacatgtacc 840
tgaaagggtcc gcgtgggttct gttatgacta ccaacatcta cctgaactct tccctgtacc 900
gtggtaccaaa attcatcatc aagaaatacg cgtctggtaa caaggacaat atcggtcgca 960
acaatgatcg tgtatacatc aatggtgtag ttaagaacaa agaataccgt ctggctacca 1020
atgcttctca ggctggtgta gaaaagatct tgtctgctct ggaaatcccg gacgttggtgta 1080
atctgtctca ggtagttgta atgaaatcca agaacgacca gggatatcact aacaaatgca 1140
aatgaatct gcaggacaac aatggtaacg atatcggttt catcggtttc caccagttca 1200
acaatatcgc taaactgggt gcttccaact ggtacaatcg tcagatcgaa cgttcctctc 1260
gcactctggg ttgctcttgg gagttcatcc cggttgatga cggttggggt gaacgtccgc 1320
tgtaaccggt gaaagctt
1338

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<210> 38

<211> 415

<212> PRT

<213> Clostridium botulinum

<400> 38

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Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys
1           5           10           15
Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln
20           25           30
Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys
35           40           45
Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe
50           55           60
Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu
65           70           75           80
Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser
85           90           95
Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile
100          105          110
Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp
115          120          125
Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn
130          135          140
Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile
145          150          155          160
Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu
165          170          175
Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Phe Tyr Phe Asn
180          185          190
Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp
195          200          205
Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu
210          215          220

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gaatagtaac ctctagagtc gaggcctgca g

1351

<210> 40

<211> 439

<212> PRT

<213> Clostridium botulinum

<400> 40

Phe	Asn	Lys	Tyr	Asn	Ser	Glu	Ile	Leu	Asn	Asn	Ile	Ile	Leu	Asn	Leu
1				5					10					15	
Arg	Tyr	Lys	Asp	Asn	Asn	Leu	Ile	Asp	Leu	Ser	Gly	Tyr	Gly	Ala	Lys
			20					25					30		
Val	Glu	Val	Tyr	Asp	Gly	Val	Glu	Leu	Asn	Asp	Lys	Asn	Gln	Phe	Lys
		35					40					45			
Leu	Thr	Ser	Ser	Ala	Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	Asn
	50					55					60				
Ile	Ile	Phe	Asn	Ser	Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	Ile
65					70				75					80	
Arg	Ile	Pro	Lys	Tyr	Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	Asn
				85					90					95	
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	Ile
			100					105					110		
Ser	Ile	Arg	Gly	Asn	Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	Gly
	115					120						125			
Lys	Thr	Lys	Ser	Val	Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	Ser
	130					135					140				
Glu	Tyr	Ile	Asn	Arg	Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu	Asn
145					150					155				160	
Asn	Ala	Lys	Ile	Tyr	Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp	Ile
				165					170					175	
Lys	Asp	Ile	Arg	Glu	Val	Ile	Ala	Asn	Gly	Glu	Ile	Ile	Phe	Lys	Leu
			180					185					190		
Asp	Gly	Asp	Ile	Asp	Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe	Ser
	195						200					205			
Ile	Phe	Asn	Thr	Glu	Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr	Lys
	210					215					220				
Ile	Gln	Ser	Tyr	Ser	Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu
225					230					235				240	
Met	Tyr	Asn	Lys	Glu	Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn	Ser
				245					250					255	
Tyr	Ile	Lys	Leu	Lys	Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr	Arg
		260						265					270		
Ser	Lys	Tyr	Asn	Gln	Asn	Ser	Lys	Tyr	Ile	Asn	Tyr	Arg	Asp	Leu	Tyr
		275					280					285			
Ile	Gly	Glu	Lys	Phe	Ile	Ile	Arg	Arg	Lys	Ser	Asn	Ser	Gln	Ser	Ile
	290					295					300				
Asn	Asp	Asp	Ile	Val	Arg	Lys	Glu	Asp	Tyr	Ile	Tyr	Leu	Asp	Phe	Phe
305					310					315				320	
Asn	Leu	Asn	Gln	Glu	Trp	Arg	Val	Tyr	Thr	Tyr	Lys	Tyr	Phe	Lys	Lys
				325					330					335	
Glu	Glu	Glu	Lys	Leu	Phe	Leu	Ala	Pro	Ile	Ser	Asp	Ser	Asp	Glu	Phe
			340					345					350		
Tyr	Asn	Thr	Ile	Gln	Ile	Lys	Glu	Tyr	Asp	Glu	Gln	Pro	Thr	Tyr	Ser
		355					360					365			
Cys	Gln	Leu	Leu	Phe	Lys	Lys	Asp	Glu	Glu	Ser	Thr	Asp	Glu	Ile	Gly
	370					375					380				
Leu	Ile	Gly	Ile	His	Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu	Glu

385 390 395 400
 Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys
 405 410 415
 Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro
 420 425 430
 Lys Asp Glu Gly Trp Thr Glu
 435

<210> 41
 <211> 848
 <212> PRT
 <213> Clostridium botulinum

<400> 41
 Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe
 1 5 10 15
 Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu
 20 25 30
 Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu
 35 40 45
 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro
 50 55 60
 Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu
 65 70 75 80
 Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu
 85 90 95
 Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu
 100 105 110
 His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu
 115 120 125
 Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys
 130 135 140
 Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu
 145 150 155 160
 Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr
 165 170 175
 Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro Ala
 180 185 190
 Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu
 195 200 205
 Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala
 210 215 220
 Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys
 225 230 235 240
 Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu
 245 250 255
 Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys
 260 265 270
 Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu
 275 280 285
 Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn
 290 295 300
 Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp
 305 310 315 320
 Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile
 325 330 335

Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	Met
			340					345					350		
Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	Lys
		355					360					365			
Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly
	370					375					380				
Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp
385					390					395					400
Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	Leu	Leu	Ser
			405						410					415	
Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn
			420					425					430		
Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser
		435					440					445			
Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn
	450					455					460				
Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu
465					470					475					480
Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser
			485						490					495	
Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn
			500					505					510		
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val
	515						520					525			
Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu
	530					535					540				
Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser
545					550					555					560
Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu
			565						570					575	
Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Pro
			580					585					590		
Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met	Phe	Lys
		595					600						605		
Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys	Tyr	Phe
	610					615					620				
Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp	Leu	Tyr
625					630					635					640
Asp	Asn	Gln	Ser	Asn	Ser	Gly	Ile	Leu	Lys	Asp	Phe	Trp	Gly	Asp	Tyr
			645						650					655	
Leu	Gln	Tyr	Asp	Lys	Pro	Tyr	Tyr	Met	Leu	Asn	Leu	Tyr	Asp	Pro	Asn
		660						665					670		
Lys	Tyr	Val	Asp	Val	Asn	Asn	Val	Gly	Ile	Arg	Gly	Tyr	Met	Tyr	Leu
	675						680					685			
Lys	Gly	Pro	Arg	Gly	Ser	Val	Met	Thr	Thr	Asn	Ile	Tyr	Leu	Asn	Ser
	690					695					700				
Ser	Leu	Tyr	Arg	Gly	Thr	Lys	Phe	Ile	Ile	Lys	Lys	Tyr	Ala	Ser	Gly
705					710					715					720
Asn	Lys	Asp	Asn	Ile	Val	Arg	Asn	Asn	Asp	Arg	Val	Tyr	Ile	Asn	Val
			725						730					735	
Val	Val	Lys	Asn	Lys	Glu	Tyr	Arg	Leu	Ala	Thr	Asn	Ala	Ser	Gln	Ala
			740					745					750		
Gly	Val	Glu	Lys	Ile	Leu	Ser	Ala	Leu	Glu	Ile	Pro	Asp	Val	Gly	Asn
	755						760					765			
Leu	Ser	Gln	Val	Val	Val	Met	Lys	Ser	Lys	Asn	Asp	Gln	Gly	Ile	Thr
	770					775					780				
Asn	Lys	Cys	Lys	Met	Asn	Leu	Gln	Asp	Asn	Asn	Gly	Asn	Asp	Ile	Gly

785					790					795				800	
Phe	Ile	Gly	Phe	His	Gln	Phe	Asn	Asn	Ile	Ala	Lys	Leu	Val	Ala	Ser
				805					810					815	
Asn	Trp	Tyr	Asn	Arg	Gln	Ile	Glu	Arg	Ser	Ser	Arg	Thr	Leu	Gly	Cys
			820					825					830		
Ser	Trp	Glu	Phe	Ile	Pro	Val	Asp	Asp	Gly	Trp	Gly	Glu	Arg	Pro	Leu
		835					840					845			

<210> 42
 <211> 850
 <212> PRT
 <213> Clostridium botulinum

<400> 42															
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			20					25				30			
Glu	Tyr	Asn	Thr	Gln	Ser	Asn	Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile	Asn
		35					40					45			
Glu	Leu	Ile	Leu	Asp	Thr	Asp	Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro	Ser
		50				55					60				
Glu	Asn	Thr	Glu	Ser	Leu	Thr	Asp	Phe	Asn	Val	Asp	Val	Pro	Val	Tyr
65					70				75					80	
Glu	Lys	Gln	Pro	Ala	Ile	Lys	Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr	Ile
				85					90					95	
Phe	Gln	Tyr	Leu	Tyr	Ser	Gln	Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp	Ile
			100					105					110		
Ser	Leu	Thr	Ser	Ser	Phe	Asp	Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys	Val
		115				120						125			
Tyr	Ser	Phe	Phe	Ser	Met	Asp	Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val	Val
		130				135					140				
Glu	Ala	Gly	Leu	Phe	Ala	Gly	Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	Phe
145					150					155					160
Val	Ile	Glu	Ala	Asn	Lys	Ser	Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	Ile
				165					170					175	
Ser	Leu	Ile	Val	Pro	Tyr	Ile	Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	Glu
		180					185					190			
Thr	Ala	Lys	Gly	Asn	Phe	Glu	Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	Ser
		195				200						205			
Ile	Leu	Leu	Glu	Phe	Ile	Pro	Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	Ala
	210					215					220				
Phe	Leu	Leu	Glu	Ser	Tyr	Ile	Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Thr
225				230						235					240
Ile	Asp	Asn	Ala	Leu	Thr	Lys	Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	Tyr
			245						250					255	
Gly	Leu	Ile	Val	Ala	Gln	Trp	Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	Tyr
			260					265					270		
Thr	Ile	Lys	Glu	Gly	Met	Tyr	Lys	Ala	Leu	Asn	Tyr	Gln	Ala	Gln	Ala
		275				280						285			
Leu	Glu	Glu	Ile	Ile	Lys	Tyr	Arg	Tyr	Asn	Ile	Tyr	Ser	Glu	Lys	Glu
	290					295					300				
Lys	Ser	Asn	Ile	Asn	Ile	Asp	Phe	Asn	Asp	Ile	Asn	Ser	Lys	Leu	Asn
305				310						315					320
Glu	Gly	Ile	Asn	Gln	Ala	Ile	Asp	Asn	Ile	Asn	Asn	Phe	Ile	Asn	Gly
			325						330					335	

Cys	Ser	Val	Ser	Tyr	Leu	Met	Lys	Lys	Met	Ile	Pro	Leu	Ala	Val	Glu
			340					345					350		
Lys	Leu	Leu	Asp	Phe	Asp	Asn	Thr	Leu	Lys	Lys	Asn	Leu	Leu	Asn	Tyr
		355					360					365			
Ile	Asp	Glu	Asn	Lys	Leu	Tyr	Leu	Ile	Gly	Ser	Ala	Glu	Tyr	Glu	Lys
	370					375					380				
Ser	Lys	Val	Asn	Lys	Tyr	Leu	Lys	Thr	Ile	Met	Pro	Phe	Asp	Leu	Ser
385					390					395					400
Ile	Tyr	Thr	Asn	Asp	Thr	Ile	Leu	Ile	Glu	Met	Phe	Asn	Lys	Tyr	Asn
			405						410					415	
Ser	Glu	Ile	Leu	Asn	Asn	Ile	Ile	Leu	Asn	Leu	Arg	Tyr	Lys	Asp	Asn
			420					425					430		
Asn	Leu	Ile	Asp	Leu	Ser	Gly	Tyr	Gly	Ala	Lys	Val	Glu	Val	Tyr	Asp
		435					440					445			
Gly	Val	Glu	Leu	Asn	Asp	Lys	Asn	Gln	Phe	Lys	Leu	Thr	Ser	Ser	Ala
	450					455					460				
Asn	Ser	Lys	Ile	Arg	Val	Thr	Gln	Asn	Gln	Asn	Ile	Ile	Phe	Asn	Ser
465					470					475					480
Val	Phe	Leu	Asp	Phe	Ser	Val	Ser	Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr
			485						490					495	
Lys	Asn	Asp	Gly	Ile	Gln	Asn	Tyr	Ile	His	Asn	Glu	Tyr	Thr	Ile	Ile
		500						505					510		
Asn	Cys	Met	Lys	Asn	Asn	Ser	Gly	Trp	Lys	Ile	Ser	Ile	Arg	Gly	Asn
		515					520					525			
Arg	Ile	Ile	Trp	Thr	Leu	Ile	Asp	Ile	Asn	Gly	Lys	Thr	Lys	Ser	Val
	530					535					540				
Phe	Phe	Glu	Tyr	Asn	Ile	Arg	Glu	Asp	Ile	Ser	Glu	Tyr	Ile	Asn	Arg
545					550					555					560
Trp	Phe	Phe	Val	Thr	Ile	Thr	Asn	Asn	Leu	Asn	Asn	Ala	Lys	Ile	Tyr
			565						570					575	
Ile	Asn	Gly	Lys	Leu	Glu	Ser	Asn	Thr	Asp	Ile	Lys	Asp	Ile	Arg	Glu
		580						585					590		
Val	Ile	Ala	Asn	Gly	Glu	Ile	Ile	Phe	Lys	Leu	Asp	Gly	Asp	Ile	Asp
		595					600					605			
Arg	Thr	Gln	Phe	Ile	Trp	Met	Lys	Tyr	Phe	Ser	Ile	Phe	Asn	Thr	Glu
	610					615					620				
Leu	Ser	Gln	Ser	Asn	Ile	Glu	Glu	Arg	Tyr	Lys	Ile	Gln	Ser	Tyr	Ser
625					630					635					640
Glu	Tyr	Leu	Lys	Asp	Phe	Trp	Gly	Asn	Pro	Leu	Met	Tyr	Asn	Lys	Glu
			645						650					655	
Tyr	Tyr	Met	Phe	Asn	Ala	Gly	Asn	Lys	Asn	Ser	Tyr	Ile	Lys	Leu	Lys
		660						665						670	
Lys	Asp	Ser	Pro	Val	Gly	Glu	Ile	Leu	Thr	Arg	Ser	Lys	Tyr	Asn	Gln
		675					680					685			
Asn	Ser														

785		790		795		800									
Arg	Phe	Tyr	Glu	Ser	Gly	Ile	Val	Phe	Glu	Glu	Tyr	Lys	Asp	Tyr	Phe
				805					810					815	
Cys	Ile	Ser	Lys	Trp	Tyr	Leu	Lys	Glu	Val	Lys	Arg	Lys	Pro	Tyr	Asn
			820					825					830		
Leu	Lys	Leu	Gly	Cys	Asn	Trp	Gln	Phe	Ile	Pro	Lys	Asp	Glu	Gly	Trp
		835					840					845			
Thr	Glu														
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 <212> PRT
 <213> Clostridium botulinum

<300>
 <308> X52066
 <309> 1993-04-23

<400> 43

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Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	Glu	Arg
		35				40					45				
Asp	Thr	Phe	Thr	Asn	Pro	Glu	Gly	Asp	Leu	Asn	Pro	Pro	Pro	Pro	Glu
	50					55				60					
Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	Tyr	Leu	Ser	Thr
65					70				75					80	
Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	Thr	Lys	Leu	Phe	Glu
				85					90					95	
Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	Leu	Leu	Thr	Ser	Ile	Val
			100					105					110		
Arg	Gly	Ile	Pro	Phe	Trp	Gly	Gly	Ser	Thr	Ile	Asp	Thr	Glu	Leu	Lys
		115				120						125			
Val	Ile	Asp	Thr	Asn	Cys	Ile	Asn	Val	Ile	Gln	Pro	Asp	Gly	Ser	Tyr
	130					135					140				
Arg	Ser	Glu	Glu	Leu	Asn	Leu	Val	Ile	Ile	Gly	Pro	Ser	Ala	Asp	Ile
145					150					155				160	
Ile	Gln	Phe	Glu	Cys	Lys	Ser	Phe	Gly	His	Glu	Val	Leu	Asn	Leu	Thr
				165					170					175	
Arg	Asn	Gly	Tyr	Gly	Ser	Thr	Gln	Tyr	Ile	Arg	Phe	Ser	Pro	Asp	Phe
		180						185					190		
Thr	Phe	Gly	Phe	Glu	Glu	Ser	Leu	Glu	Val	Asp	Thr	Asn	Pro	Leu	Leu
		195					200					205			
Gly	Ala	Gly	Lys	Phe	Ala	Thr	Asp	Pro	Ala	Val	Thr	Leu	Ala	His	Glu
	210					215					220				
Leu	Ile	His	Ala	Gly	His	Arg	Leu	Tyr	Gly	Ile	Ala	Ile	Asn	Pro	Asn
225					230					235				240	
Arg	Val	Phe	Lys	Val	Asn	Thr	Asn	Ala	Tyr	Tyr	Glu	Met	Ser	Gly	Leu
				245					250					255	
Glu	Val	Ser	Phe	Glu	Glu	Leu	Arg	Thr	Phe	Gly	Gly	His	Asp	Ala	Lys
			260					265					270		
Phe	Ile	Asp	Ser	Leu	Gln	Glu	Asn	Glu	Phe	Arg	Leu	Tyr	Tyr	Tyr	Asn
		275					280					285			

Lys	Phe	Lys	Asp	Ile	Ala	Ser	Thr	Leu	Asn	Lys	Ala	Lys	Ser	Ile	Val
290						295					300				
Gly	Thr	Thr	Ala	Ser	Leu	Gln	Tyr	Met	Lys	Asn	Val	Phe	Lys	Glu	Lys
305					310					315					320
Tyr	Leu	Leu	Ser	Glu	Asp	Thr	Ser	Gly	Lys	Phe	Ser	Val	Asp	Lys	Leu
				325					330					335	
Lys	Phe	Asp	Lys	Leu	Tyr	Lys	Met	Leu	Thr	Glu	Ile	Tyr	Thr	Glu	Asp
			340					345					350		
Asn	Phe	Val	Lys	Phe	Phe	Lys	Val	Leu	Asn	Arg	Lys	Thr	Tyr	Leu	Asn
		355					360					365			
Phe	Asp	Lys	Ala	Val	Phe	Lys	Ile	Asn	Ile	Val	Pro	Lys	Val	Asn	Tyr
	370					375					380				
Thr	Ile	Tyr	Asp	Gly	Phe	Asn	Leu	Arg	Asn	Thr	Asn	Leu	Ala	Ala	Asn
385					390					395					400
Phe	Asn	Gly	Gln	Asn	Thr	Glu	Ile	Asn	Asn	Met	Asn	Phe	Thr	Lys	Leu
				405					410					415	
Lys	Asn	Phe	Thr	Gly	Leu	Phe	Glu	Phe	Tyr	Lys	Leu	Leu	Cys	Val	Arg
			420					425					430		
Gly	Ile	Ile	Thr	Ser	Lys	Thr	Lys	Ser	Leu	Asp	Lys	Gly	Tyr	Asn	Lys
		435					440					445			
Ala	Leu	Asn	Asp	Leu	Cys	Ile	Lys	Val	Asn	Asn	Trp	Asp	Leu	Phe	Phe
	450					455					460				
Ser	Pro	Ser	Glu	Asp	Asn	Phe	Thr	Asn	Asp	Leu	Asn	Lys	Gly	Glu	Glu
465					470					475					480
Ile	Thr	Ser	Asp	Thr	Asn	Ile	Glu	Ala	Ala	Glu	Glu	Asn	Ile	Ser	Leu
				485					490					495	
Asp	Leu	Ile	Gln	Tyr	Tyr	Leu	Thr	Phe	Asn	Phe	Asp	Asn	Glu	Pro	
			500					505					510		
Glu	Asn	Ile	Ser	Ile	Glu	Asn	Leu	Ser	Ser	Asp	Ile	Ile	Gly	Gln	Leu
		515					520					525			
Glu	Leu	Met	Pro	Asn	Ile	Glu	Arg	Phe	Pro	Asn	Gly	Lys	Lys	Tyr	Glu
	530					535					540				
Leu	Asp	Lys	Tyr	Thr	Met	Phe	His	Tyr	Leu	Arg	Ala	Gln	Glu	Phe	Glu
545					550					555					560
His	Gly	Lys	Ser	Arg	Ile	Ala	Leu	Thr	Asn	Ser	Val	Asn	Glu	Ala	Leu
				565						570				575	
Leu	Asn	Pro	Ser	Arg	Val	Tyr	Thr	Phe	Phe	Ser	Ser	Asp	Tyr	Val	Lys
			580					585					590		
Lys	Val	Asn	Lys	Ala	Thr	Glu	Ala	Ala	Met	Phe	Leu	Gly	Trp	Val	Glu
		595					600					605			
Gln	Leu	Val	Tyr	Asp	Phe	Thr	Asp	Glu	Thr	Ser	Glu	Val	Ser	Thr	Thr
	610					615					620				
Asp	Lys	Ile	Ala	Asp	Ile	Thr	Ile	Ile	Ile	Pro	Tyr	Ile	Gly	Pro	Ala
625					630					635					640
Leu															

			740					745					750			
Gln	Tyr	Thr	Glu	Glu	Glu	Lys	Asn	Asn	Ile	Asn	Phe	Asn	Ile	Asp	Asp	
		755					760					765				
Leu	Ser	Ser	Lys	Leu	Asn	Glu	Ser	Ile	Asn	Lys	Ala	Met	Ile	Asn	Ile	
	770					775					780					
Asn	Lys	Phe	Leu	Asn	Gln	Cys	Ser	Val	Ser	Tyr	Leu	Met	Asn	Ser	Met	
785					790					795					800	
Ile	Pro	Tyr	Gly	Val	Lys	Arg	Leu	Glu	Asp	Phe	Asp	Ala	Ser	Leu	Lys	
			805						810					815		
Asp	Ala	Leu	Leu	Lys	Tyr	Ile	Tyr	Asp	Asn	Arg	Gly	Thr	Leu	Ile	Gly	
		820						825					830			
Gln	Val	Asp	Arg	Leu	Lys	Asp	Lys	Val	Asn	Asn	Thr	Leu	Ser	Thr	Asp	
		835					840					845				
Ile	Pro	Phe	Gln	Leu	Ser	Lys	Tyr	Val	Asp	Asn	Gln	Arg	Leu	Leu	Ser	
	850					855					860					
Thr	Phe	Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	
865					870					875					880	
Leu	Arg	Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	
			885						890					895		
Lys	Ile	Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	
		900						905				910				
Gln	Ile	Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	
		915					920					925				
Lys	Asn	Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	
	930					935					940					
Phe	Trp	Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	
945					950					955					960	
Glu	Tyr	Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	
			965						970					975		
Ser	Leu	Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	
			980					985					990			
Ile	Lys	Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser	
		995					1000					1005				
Asp	Tyr	Ile	Asn	Arg	Trp	Ile	Phe	Val	Thr	Ile	Thr	Asn	Asn	Arg	Leu	
	1010					1015					1020					
Asn	Asn	Ser	Lys	Ile	Tyr	Ile	Asn	Gly	Arg	Leu	Ile	Asp	Gln	Lys	Pro	
1025					1030					1035					1040	
Ile	Ser	Asn	Leu	Gly	Asn	Ile	His	Ala	Ser	Asn	Asn	Ile	Met	Phe	Lys	
			1045						1050					1055		
Leu	Asp	Gly	Cys	Arg	Asp	Thr	His	Arg	Tyr	Ile	Trp	Ile	Lys	Tyr	Phe	
		1060						1065				1070				
Asn	Leu	Phe	Asp	Lys	Glu	Leu	Asn	Glu	Lys	Glu	Ile	Lys	Asp	Leu	Tyr	
		1075					1080				1085					
Asp	Asn	Gln	Ser													

Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn
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 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr
 1220 1225 1230
 Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly
 1235 1240 1245
 Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser
 1250 1255 1260
 Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys
 1265 1270 1275 1280
 Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu
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<210> 44
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<300>
 <308> M81186
 <309> 1993-04-26

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 Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu
 35 40 45
 Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly
 50 55 60
 Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn
 65 70 75 80
 Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe
 85 90 95
 Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile
 100 105 110
 Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu
 115 120 125
 Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn
 130 135 140
 Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile
 145 150 155 160
 Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly
 165 170 175
 Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln
 180 185 190
 Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu
 195 200 205
 Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro
 210 215 220
 Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr
 225 230 235 240
 Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe
 245 250 255
 Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe

				260					265				270				
Gly	Gly	Gln	Asp	Pro	Ser	Ile	Ile	Thr	Pro	Ser	Thr	Asp	Lys	Ser	Ile		
		275					280					285					
Tyr	Asp	Lys	Val	Leu	Gln	Asn	Phe	Arg	Gly	Ile	Val	Asp	Arg	Leu	Asn		
	290					295					300						
Lys	Val	Leu	Val	Cys	Ile	Ser	Asp	Pro	Asn	Ile	Asn	Ile	Asn	Ile	Tyr		
305					310					315					320		
Lys	Asn	Lys	Phe	Lys	Asp	Lys	Tyr	Lys	Phe	Val	Glu	Asp	Ser	Glu	Gly		
			325						330					335			
Lys	Tyr	Ser	Ile	Asp	Val	Glu	Ser	Phe	Asp	Lys	Leu	Tyr	Lys	Ser	Leu		
		340						345					350				
Met	Phe	Gly	Phe	Thr	Glu	Thr	Asn	Ile	Ala	Glu	Asn	Tyr	Lys	Ile	Lys		
	355					360					365						
Thr	Arg	Ala	Ser	Tyr	Phe	Ser	Asp	Ser	Leu	Pro	Pro	Val	Lys	Ile	Lys		
	370					375					380						
Asn	Leu	Leu	Asp	Asn	Glu	Ile	Tyr	Thr	Ile	Glu	Glu	Gly	Phe	Asn	Ile		
385				390						395					400		
Ser	Asp	Lys	Asp	Met	Glu	Lys	Glu	Tyr	Arg	Gly	Gln	Asn	Lys	Ala	Ile		
			405					410						415			
Asn	Lys	Gln	Ala	Tyr	Glu	Glu	Ile	Ser	Lys	Glu	His	Leu	Ala	Val	Tyr		
		420						425					430				
Lys	Ile	Gln	Met	Cys	Lys	Ser	Val	Lys	Ala	Pro	Gly	Ile	Cys	Ile	Asp		
	435					440					445						
Val	Asp	Asn	Glu	Asp	Leu	Phe	Phe	Ile	Ala	Asp	Lys	Asn	Ser	Phe	Ser		
	450					455				460							
Asp	Asp	Leu	Ser	Lys	Asn	Glu	Arg	Ile	Glu	Tyr	Asn	Thr	Gln	Ser	Asn		
465				470					475						480		
Tyr	Ile	Glu	Asn	Asp	Phe	Pro	Ile	Asn	Glu	Leu	Ile	Leu	Asp	Thr	Asp		
			485					490					495				
Leu	Ile	Ser	Lys	Ile	Glu	Leu	Pro	Ser	Glu	Asn	Thr	Glu	Ser	Leu	Thr		
		500						505					510				
Asp	Phe	Asn	Val	Asp	Val	Pro	Val	Tyr	Glu	Lys	Gln	Pro	Ala	Ile	Lys		
	515						520					525					
Lys	Ile	Phe	Thr	Asp	Glu	Asn	Thr	Ile	Phe	Gln	Tyr	Leu	Tyr	Ser	Gln		
	530					535					540						
Thr	Phe	Pro	Leu	Asp	Ile	Arg	Asp	Ile	Ser	Leu	Thr	Ser	Ser	Phe	Asp		
545					550					555					560		
Asp	Ala	Leu	Leu	Phe	Ser	Asn	Lys	Val	Tyr	Ser	Phe	Phe	Ser	Met	Asp		
			565					570					575				
Tyr	Ile	Lys	Thr	Ala	Asn	Lys	Val	Val	Glu	Ala	Gly	Leu	Phe	Ala	Gly		
		580						585					590				
Trp	Val	Lys	Gln	Ile	Val	Asn	Asp	Phe	Val	Ile	Glu	Ala	Asn	Lys	Ser		
	595					600						605					
Asn	Thr	Met	Asp	Lys	Ile	Ala	Asp	Ile	Ser	Leu	Ile	Val	Pro	Tyr	Ile		
	610					615					620						
Gly	Leu	Ala	Leu	Asn	Val	Gly	Asn	Glu	Thr	Ala	Lys	Gly	Asn	Phe	Glu		
625				630						635					640		
Asn	Ala	Phe	Glu	Ile	Ala	Gly	Ala	Ser	Ile	Leu	Leu	Glu	Phe	Ile	Pro		
			645					650					655				
Glu	Leu	Leu	Ile	Pro	Val	Val	Gly	Ala	Phe	Leu	Leu	Glu	Ser	Tyr	Ile		
		660						665					670				
Asp	Asn	Lys	Asn	Lys	Ile	Ile	Lys	Thr	Ile	Asp	Asn	Ala	Leu	Thr	Lys		
	675						680					685					
Arg	Asn	Glu	Lys	Trp	Ser	Asp	Met	Tyr	Gly	Leu	Ile	Val	Ala	Gln	Trp		
	690					695					700						
Leu	Ser	Thr	Val	Asn	Thr	Gln	Phe	Tyr	Thr	Ile	Lys	Glu	Gly	Met	Tyr		
705					710					715					720		

Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr
 725 730 735
 Arg Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp
 740 745 750
 Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile
 755 760 765
 Asp Asn Ile Asn Asn Phe Ile Asn Gly Cys Ser Val Ser Tyr Leu Met
 770 775 780
 Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn
 785 790 795 800
 Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr
 805 810 815
 Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asn Lys Tyr Leu
 820 825 830
 Lys Thr Ile Met Pro Phe Asp Leu Ser Ile Tyr Thr Asn Asp Thr Ile
 835 840 845
 Leu Ile Glu Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile
 850 855 860
 Ile Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly
 865 870 875 880
 Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys
 885 890 895
 Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr
 900 905 910
 Gln Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val
 915 920 925
 Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn
 930 935 940
 Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser
 945 950 955 960
 Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile
 965 970 975
 Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg
 980 985 990
 Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr
 995 1000 1005
 Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser
 1010 1015 1020
 Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile
 1025 1030 1035 1040
 Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met
 1045 1050 1055
 Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu
 1060 1065 1070
 Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp
 1075 1080 1085
 Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly
 1090 1095 1100
 Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu
 1105 1110 1115 1120
 Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr
 1125 1130 1135
 Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn
 1140 1145 1150
 Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr
 1155 1160 1165
 Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys

1170	1175	1180
Tyr Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp		
1185	1190	1195
Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln		1200
	1205	1210
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr		1215
	1220	1225
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile		1230
	1235	1240
Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu		1245
	1250	1255
Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp		1260
1265	1270	1275
Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu		1280
	1285	1290

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